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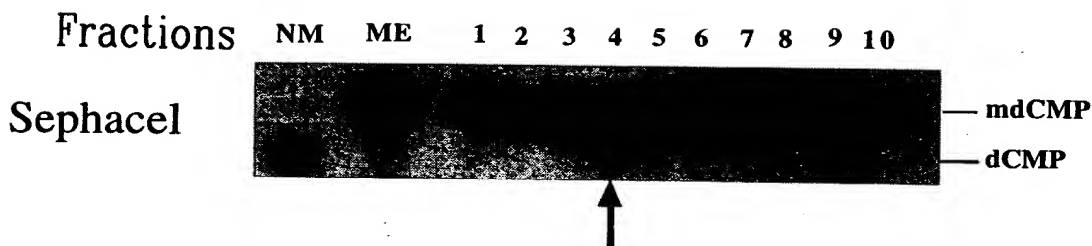
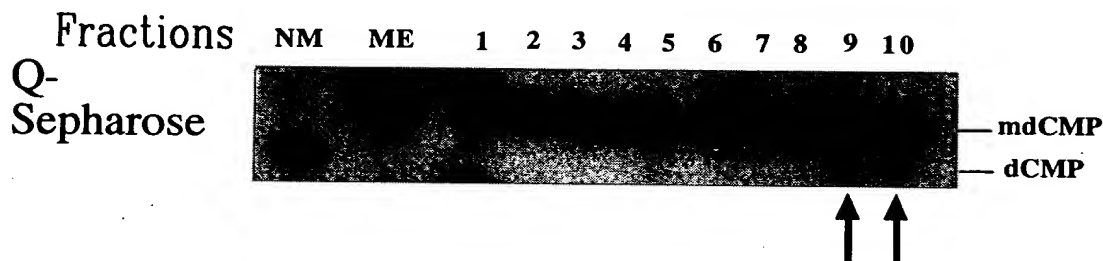
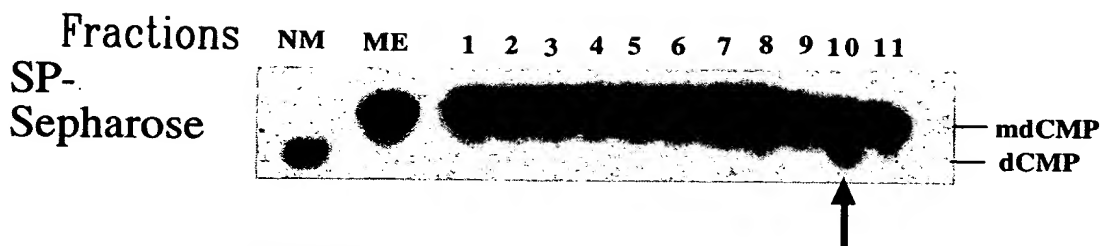
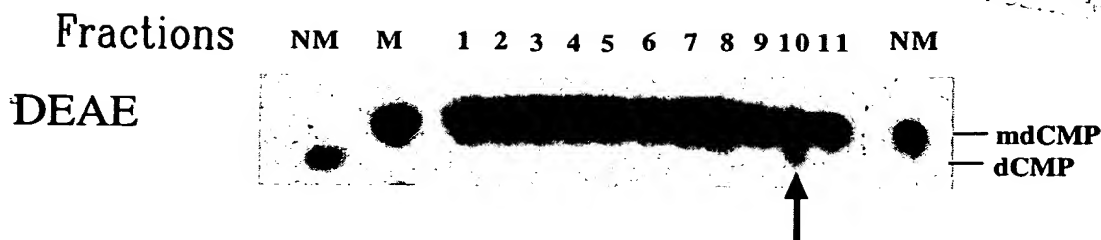
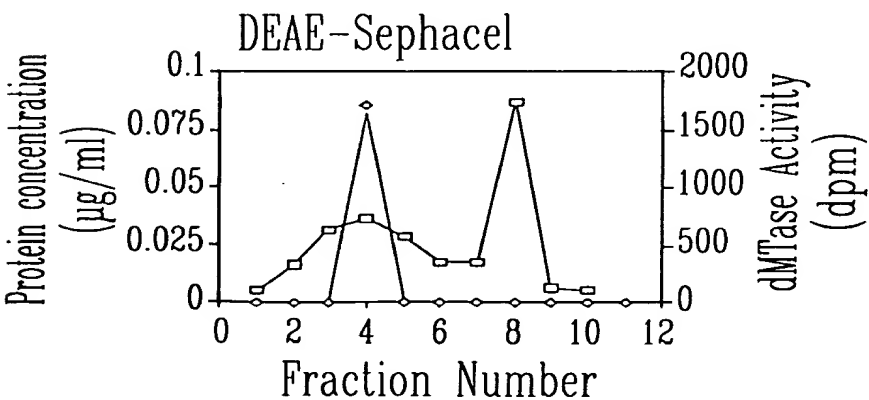
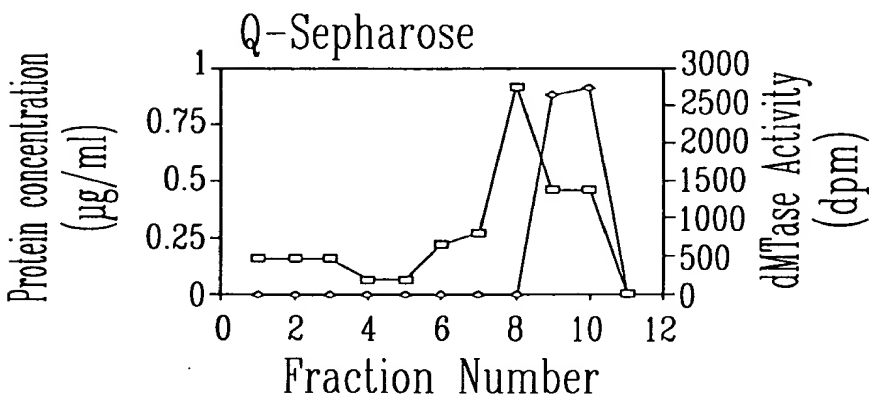
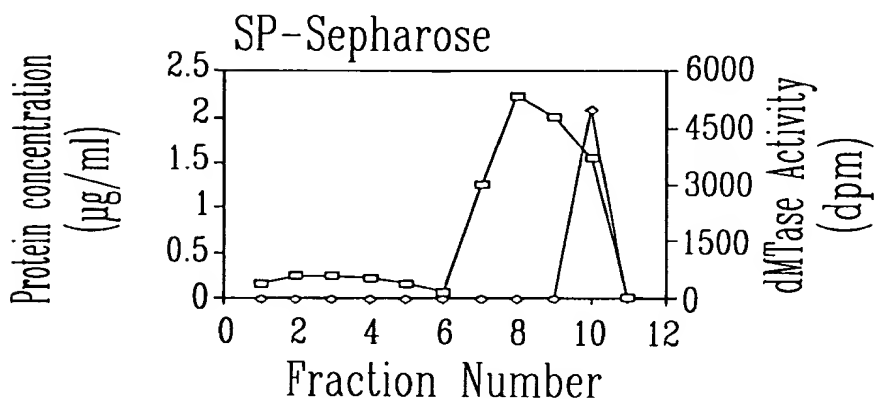
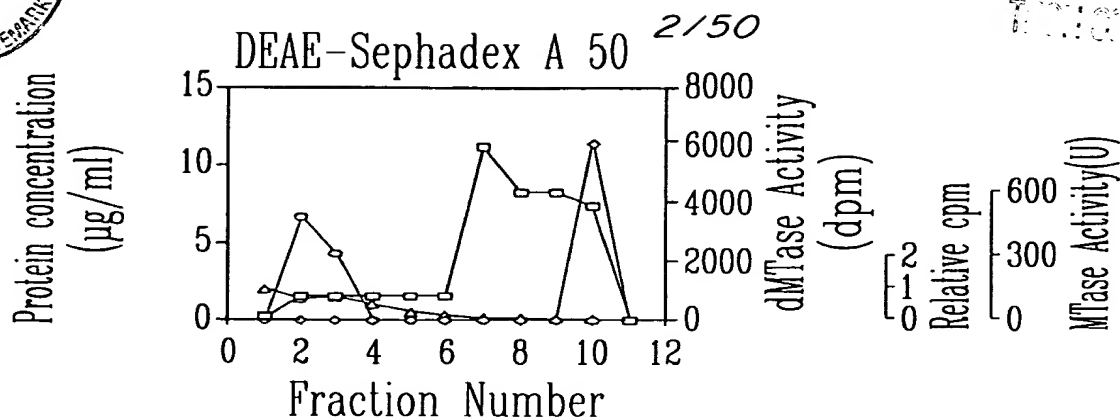


FIG. 1A



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FIG. 1





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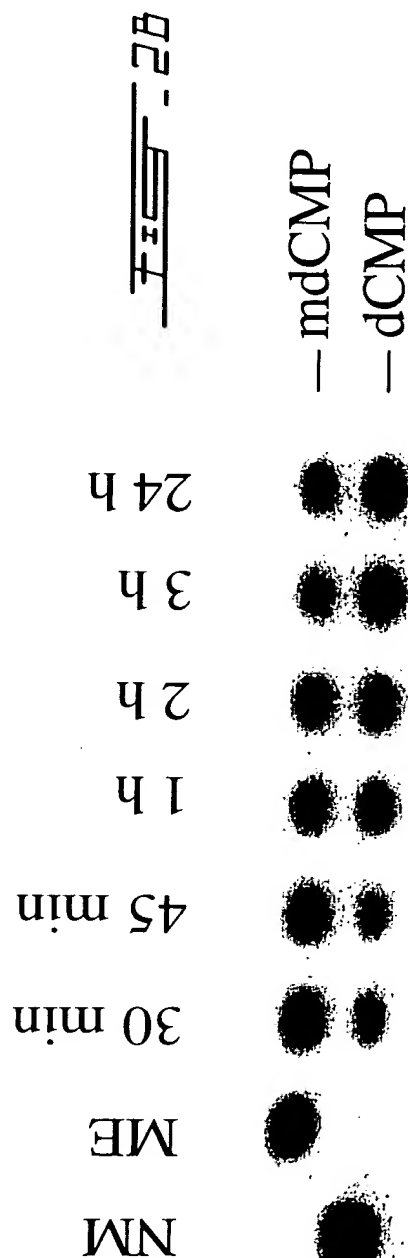
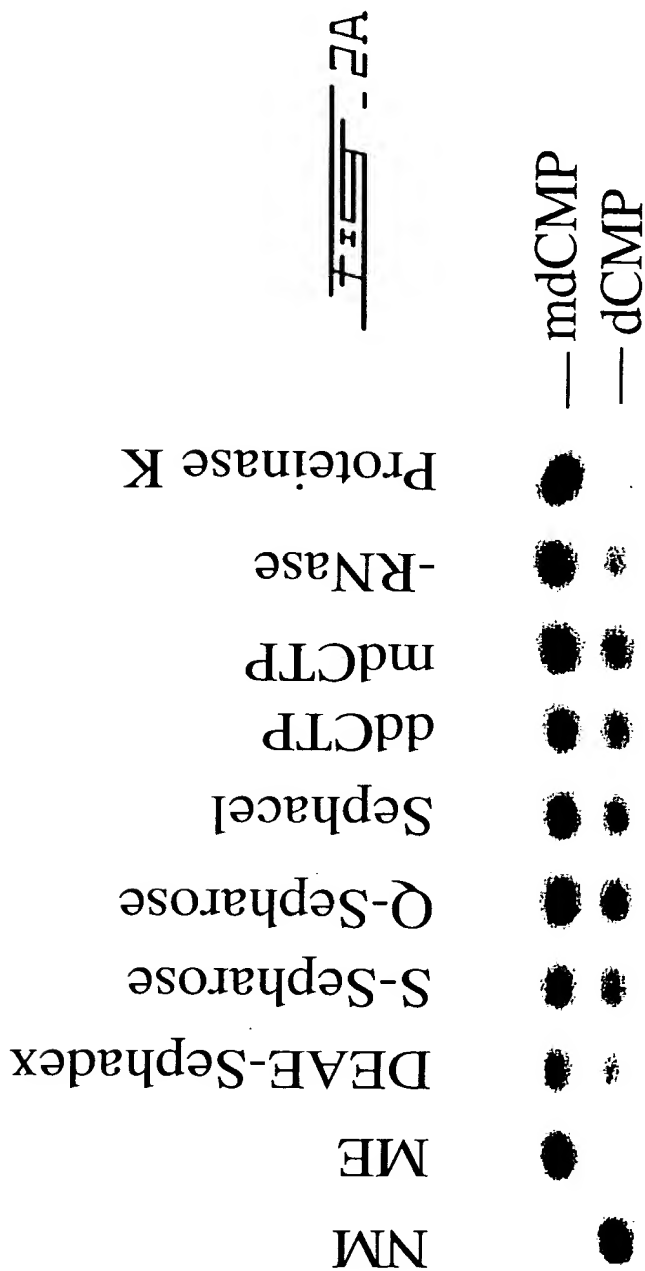




FIGURE 2

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FIGURE 2

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picomole cytosine formed

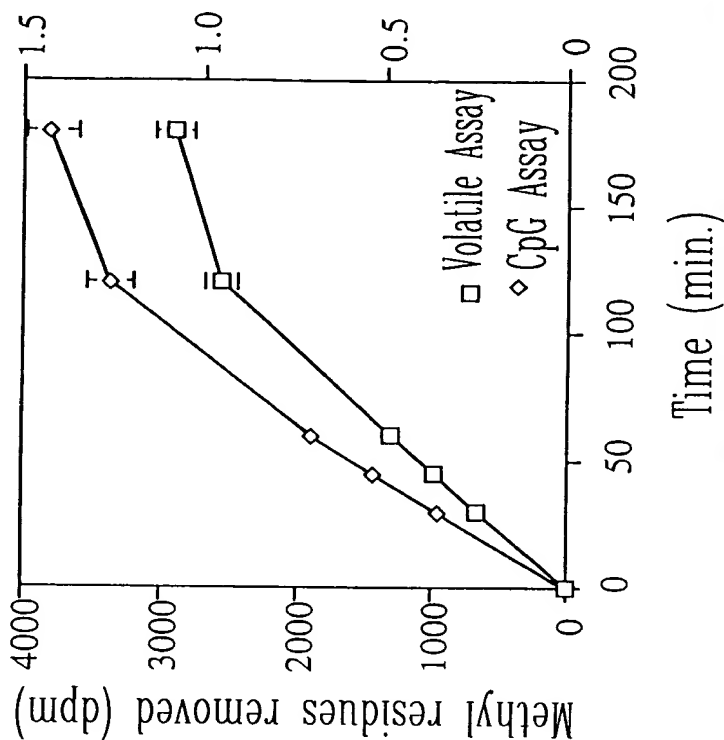


FIGURE 2

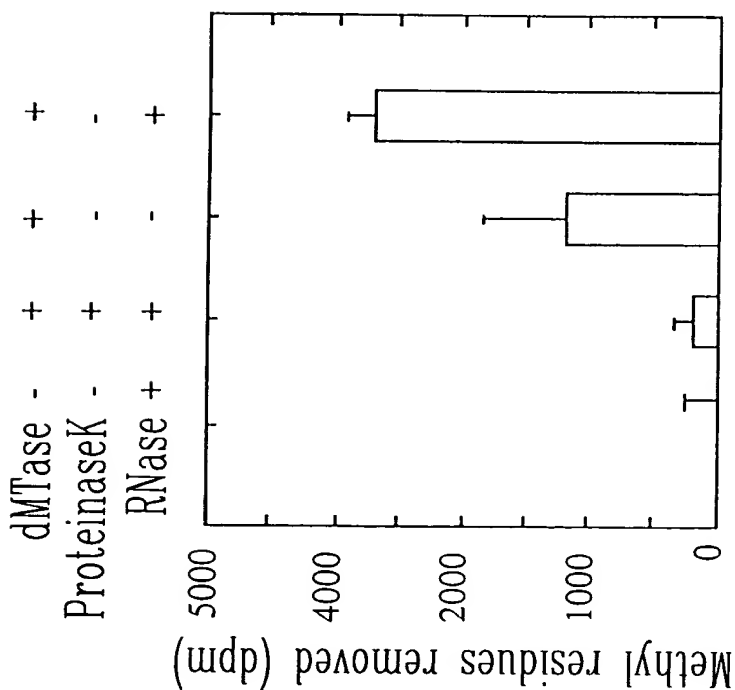


FIGURE 2



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FIG. 3A

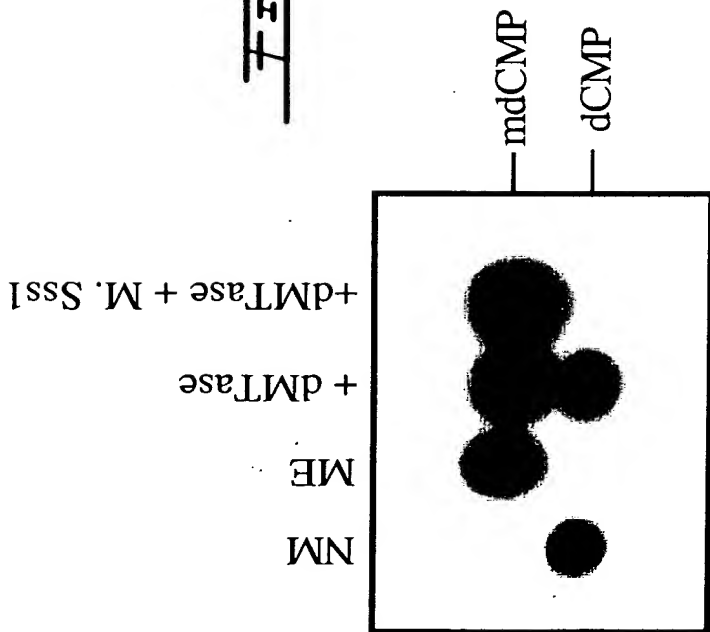
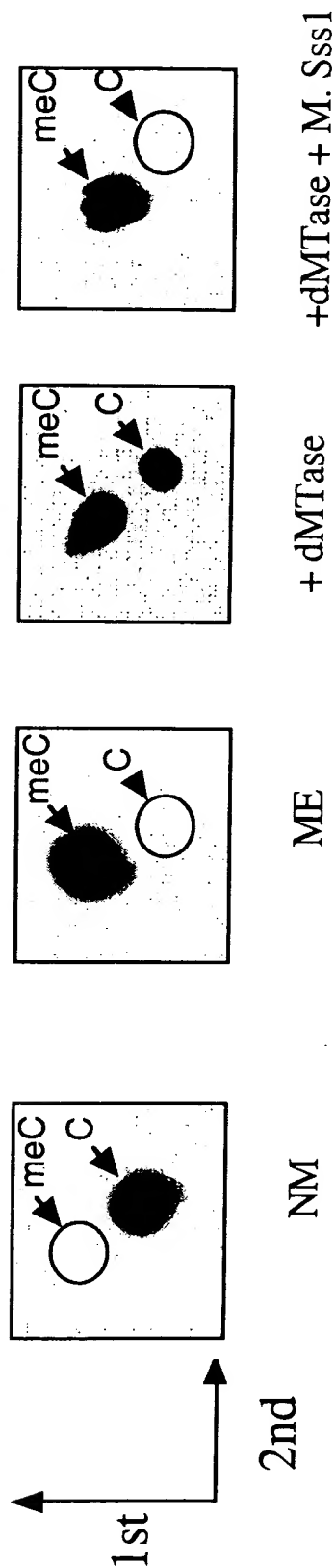


FIG. 3B

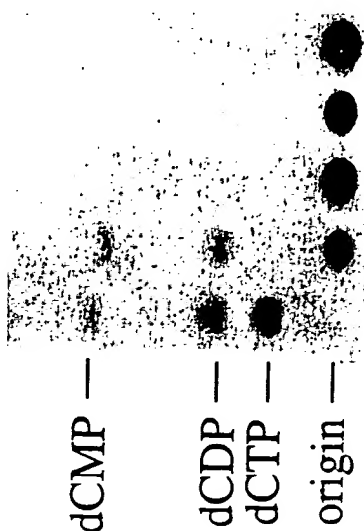




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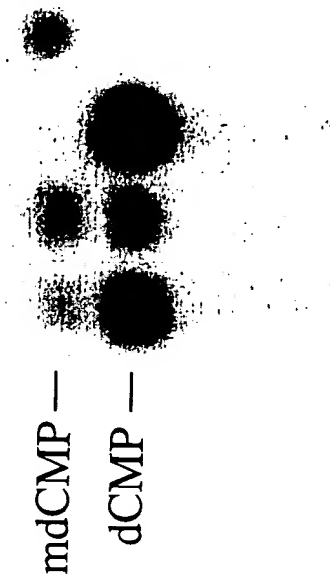
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- V PDS  
dCTP  
N.E.  
0  
60  
120



+ V PDS

+RNase  
-RNase  
NM  
ME



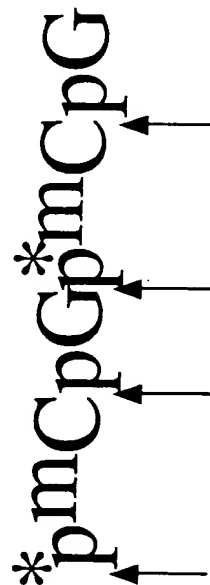
- V PDS  
dGTP  
N.E.  
0  
60  
120  
+RNase



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Labeled nucleotide:  
[ $\alpha$ 32P]-dCTP

Labeled nucleotide:  
[ $\alpha$ 32P]-dGTP



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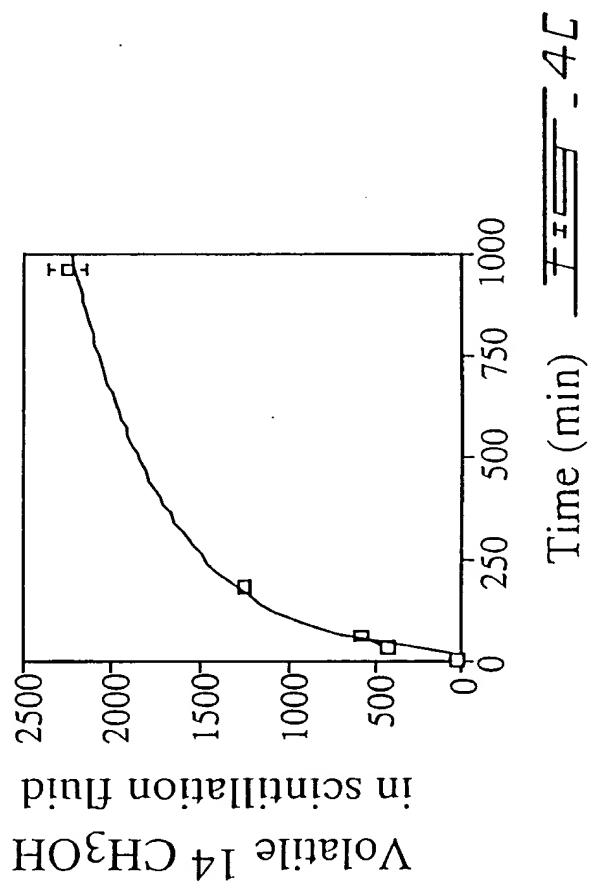
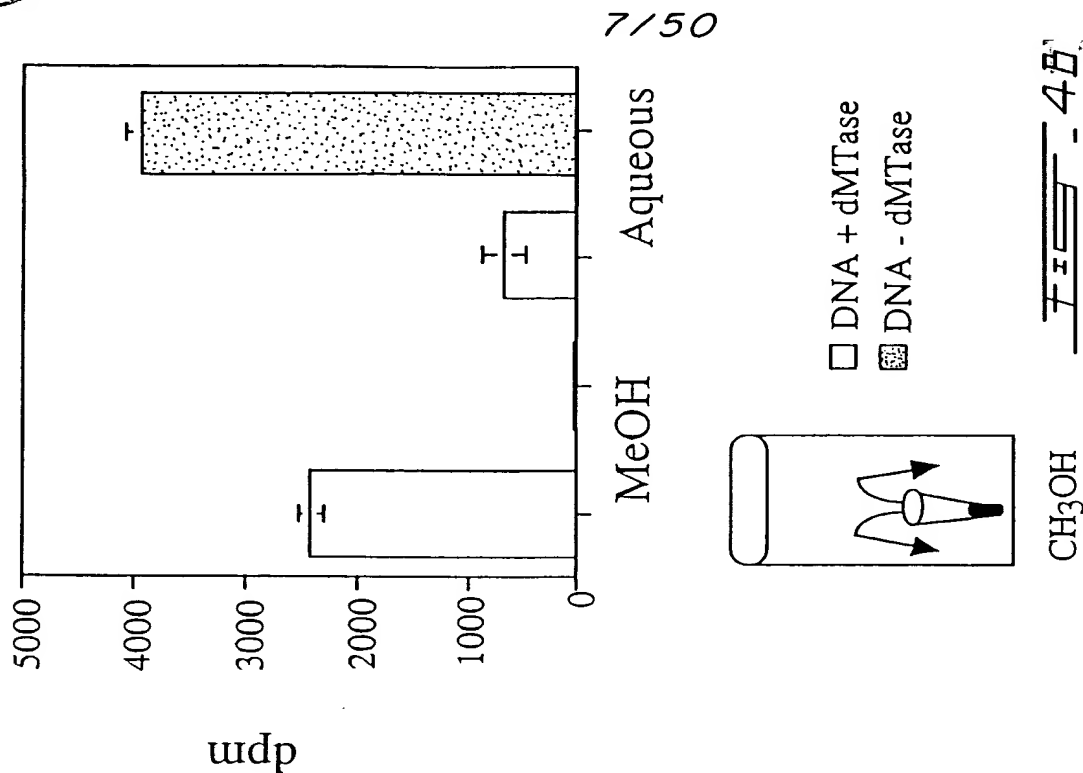
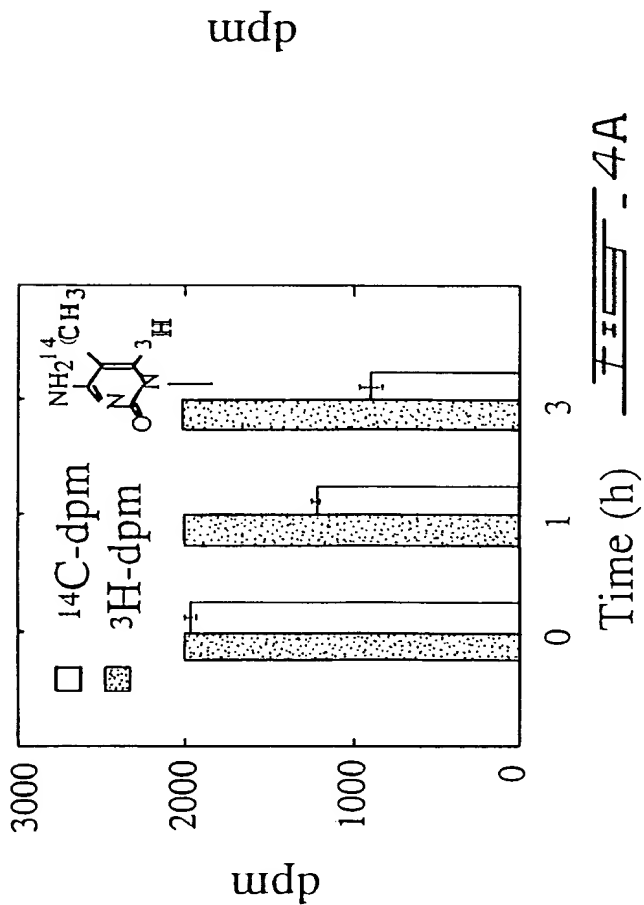




FIGURE 10

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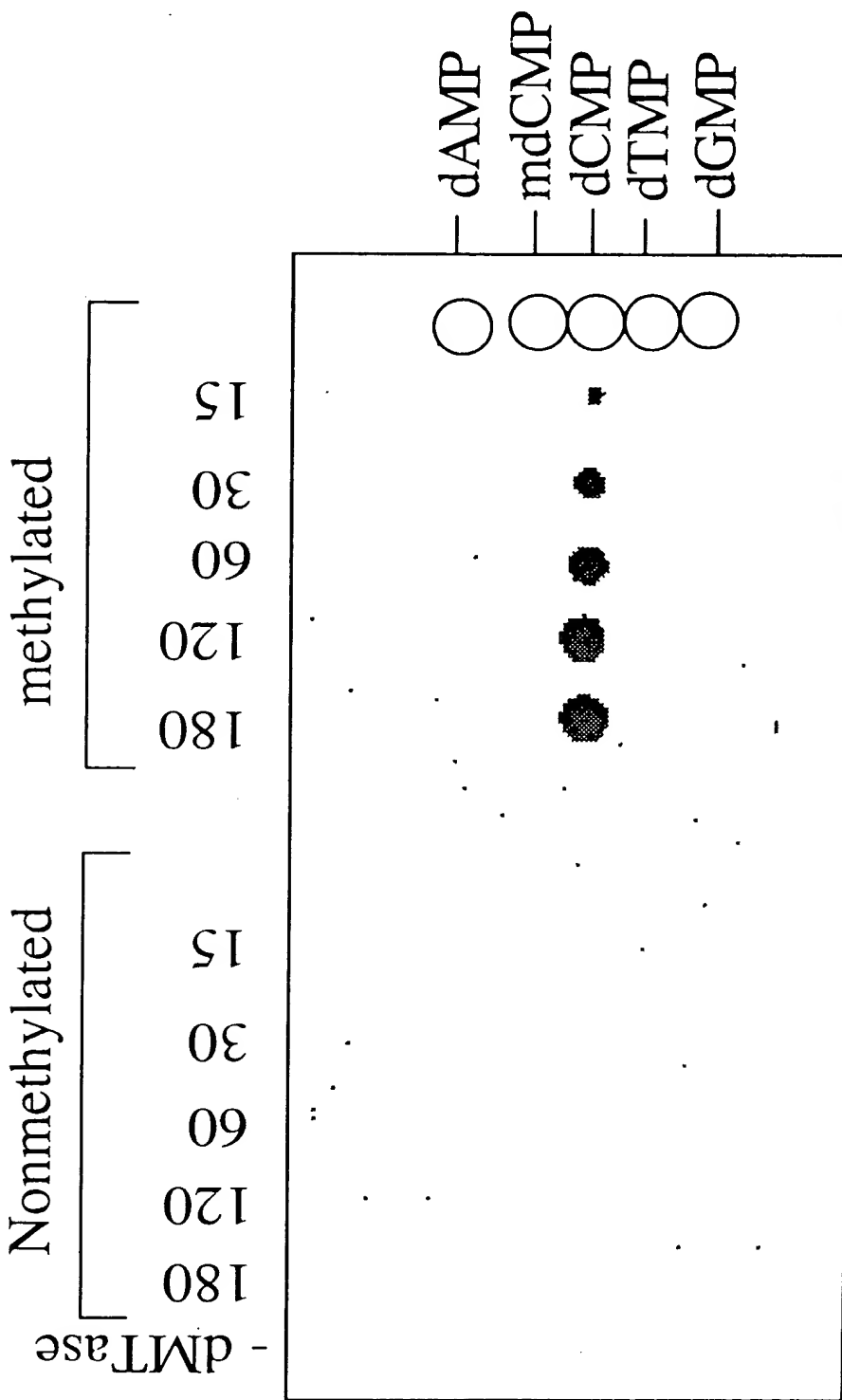


Fig. 10

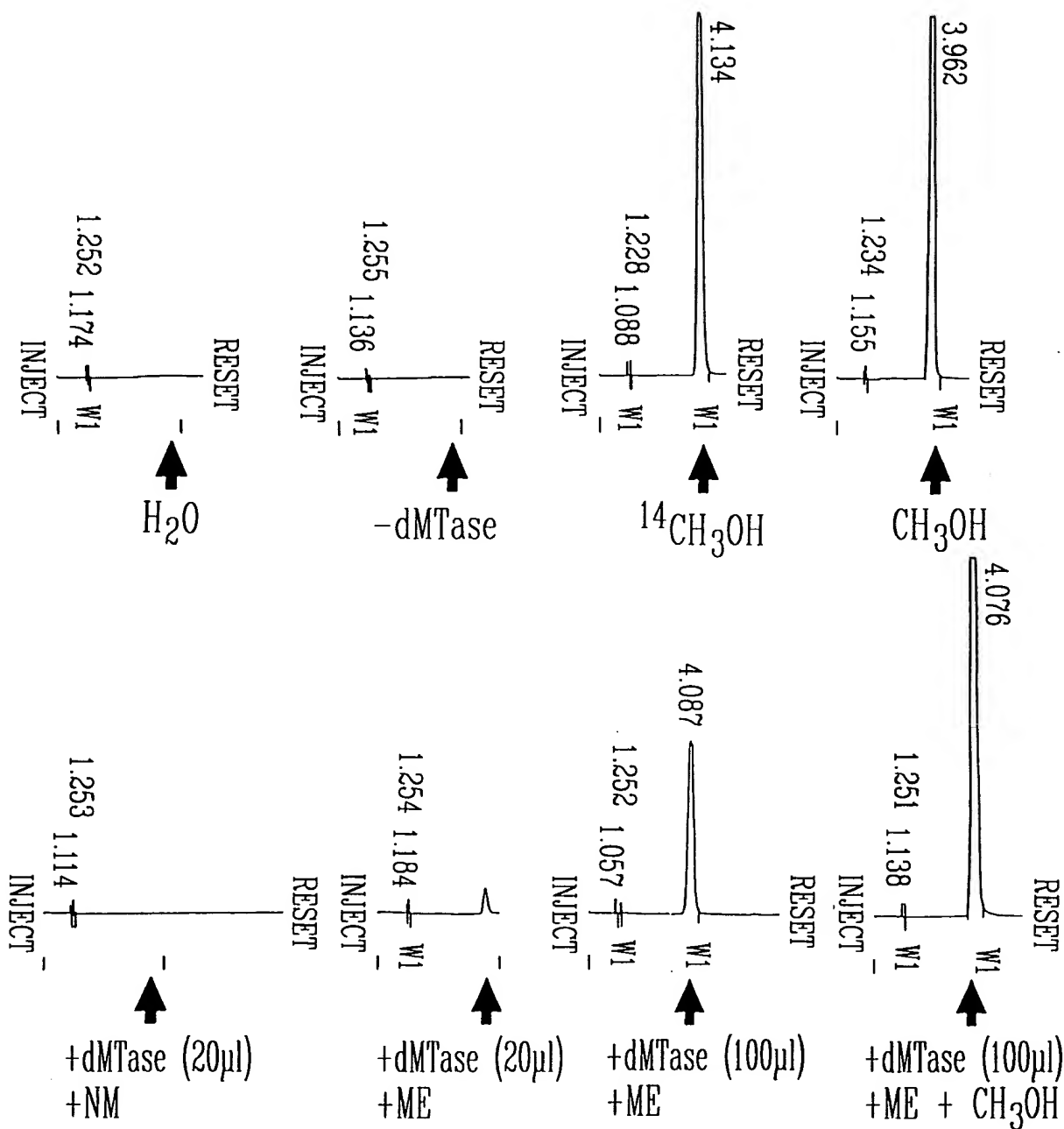


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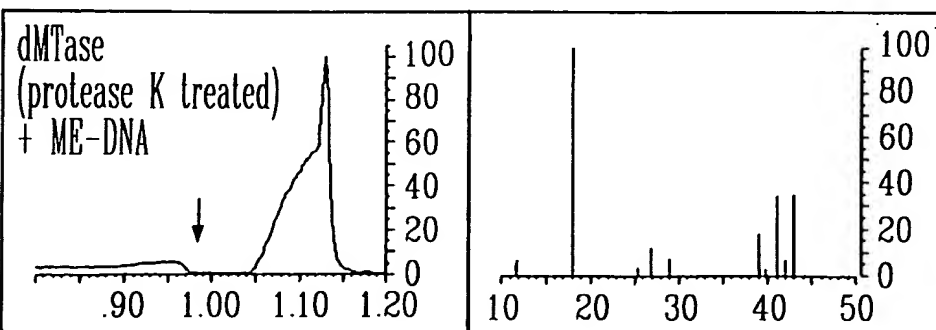
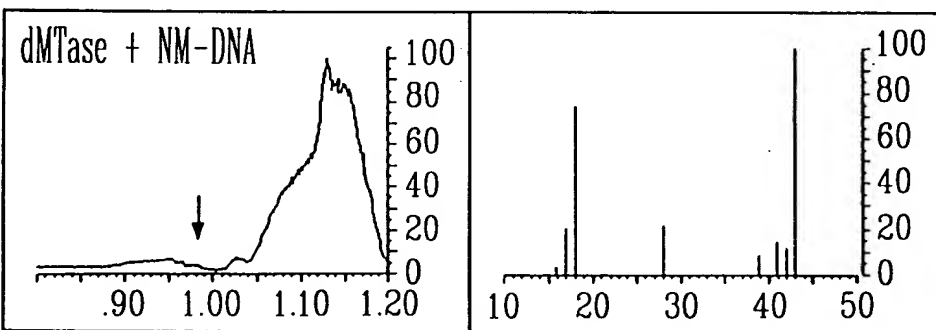
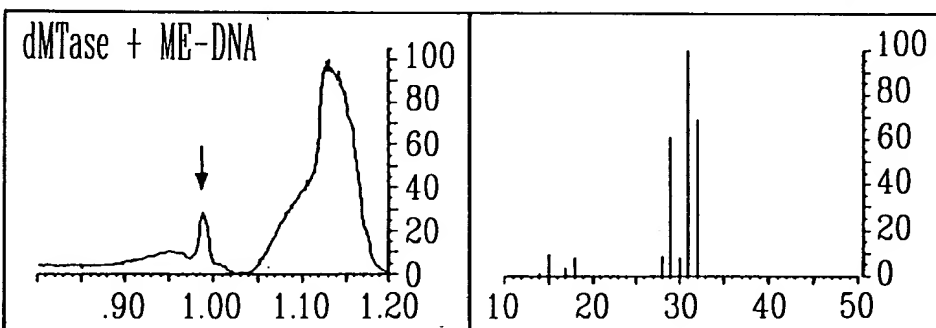
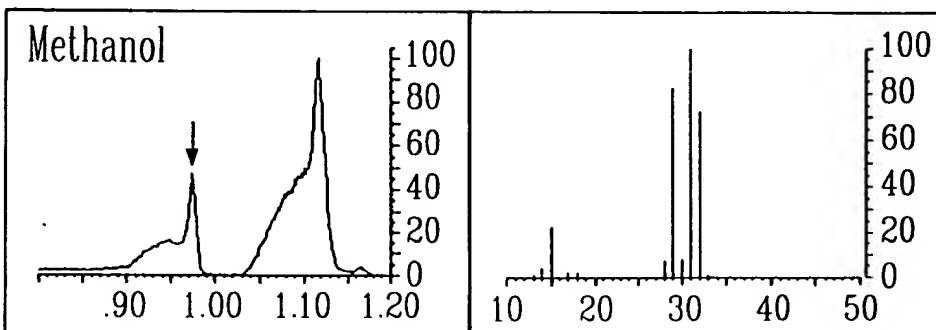
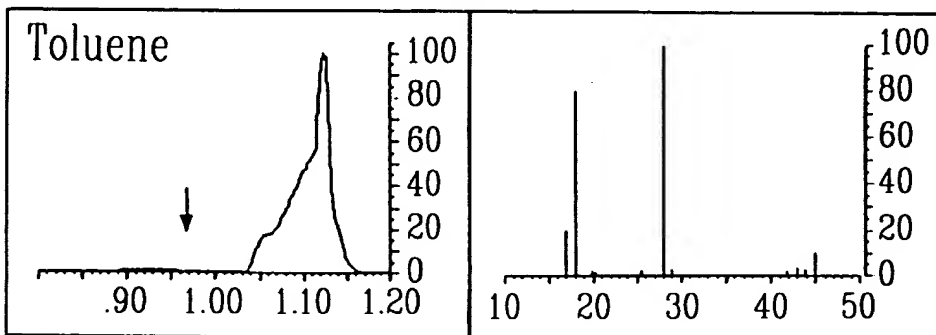
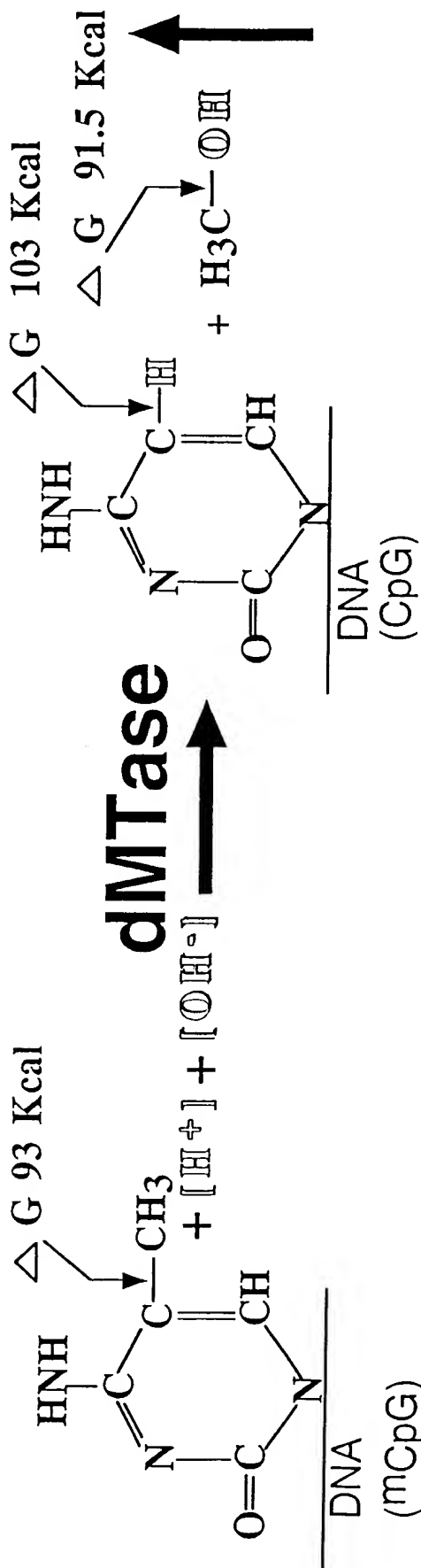


FIG. 4F

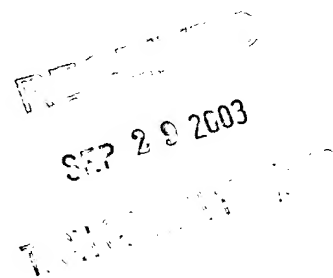


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$$\Delta G_{\text{Reaction}} = (93) - (103 + 91.5) = (-101.5) \text{ Kcal}$$

Fig. 5





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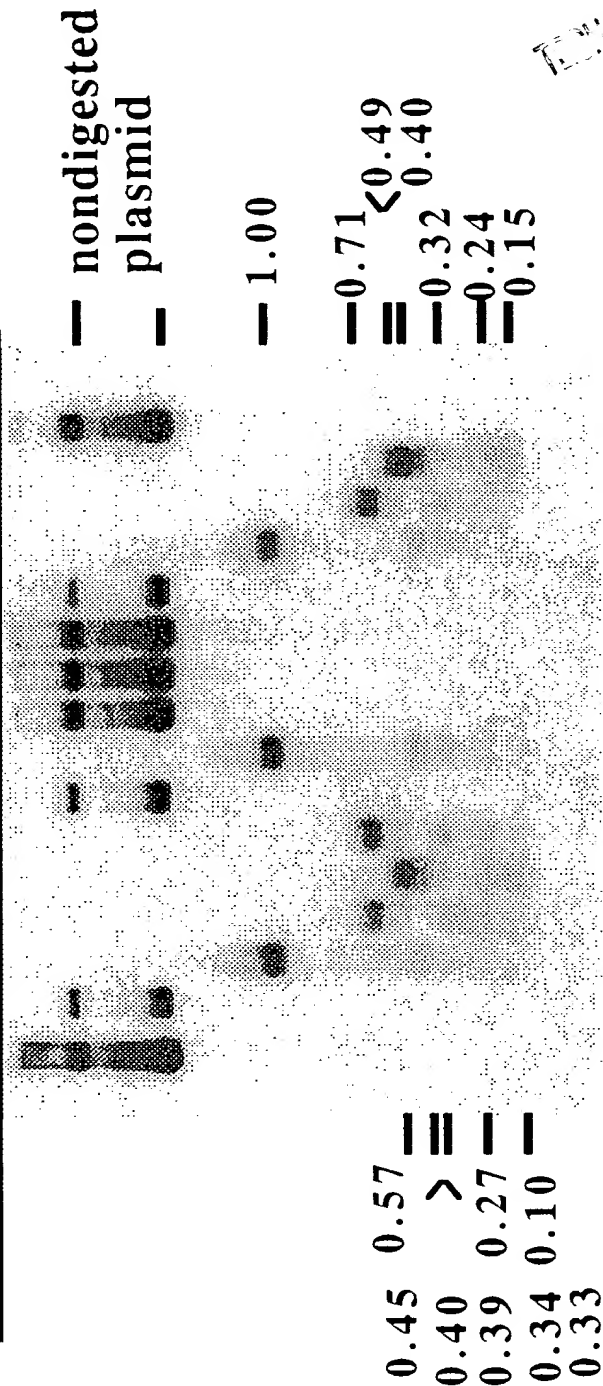
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M.MspI+M.SssI      -      +      +      +

dMTase      -      -      -      +

--	--	--	--	--

EcoRII	+	+	+	+
DpnI	+	+	+	+
HpaII	+	+	+	+
HhaI	+	+	+	+
MspI	+	+	+	+



FEES - BA

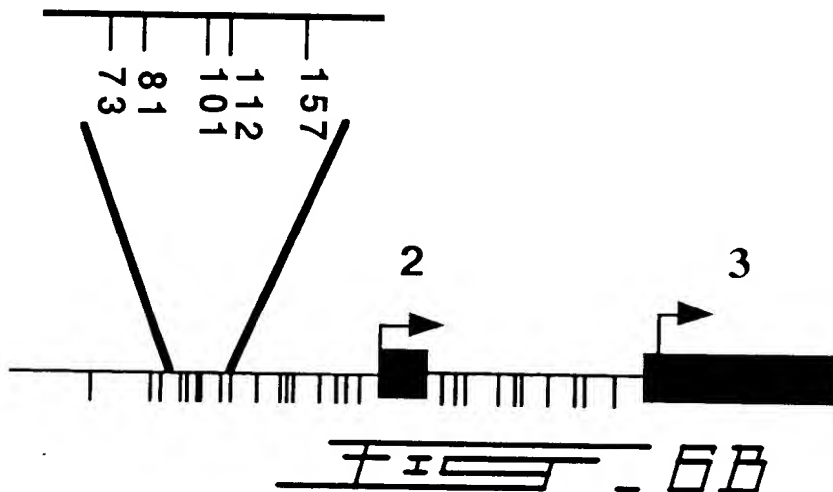
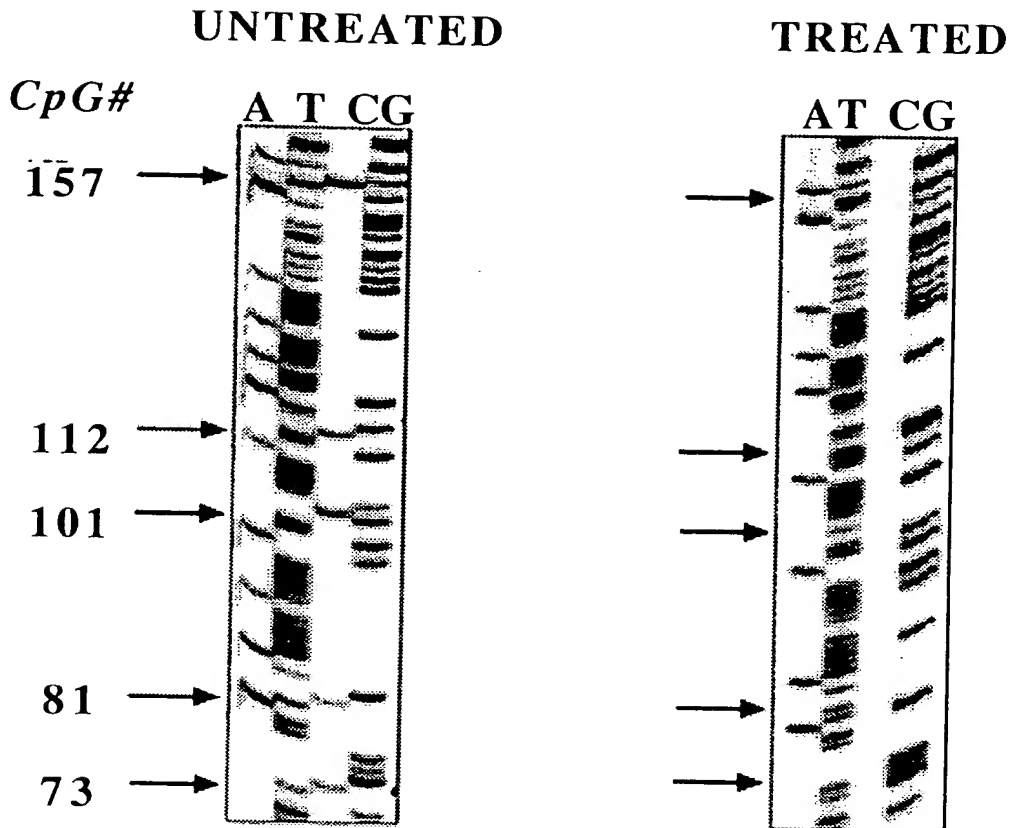


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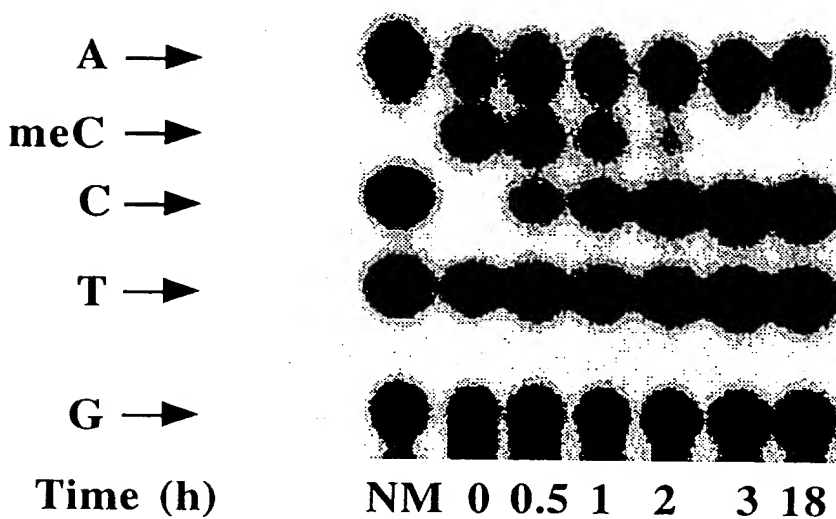


FIG. 1B

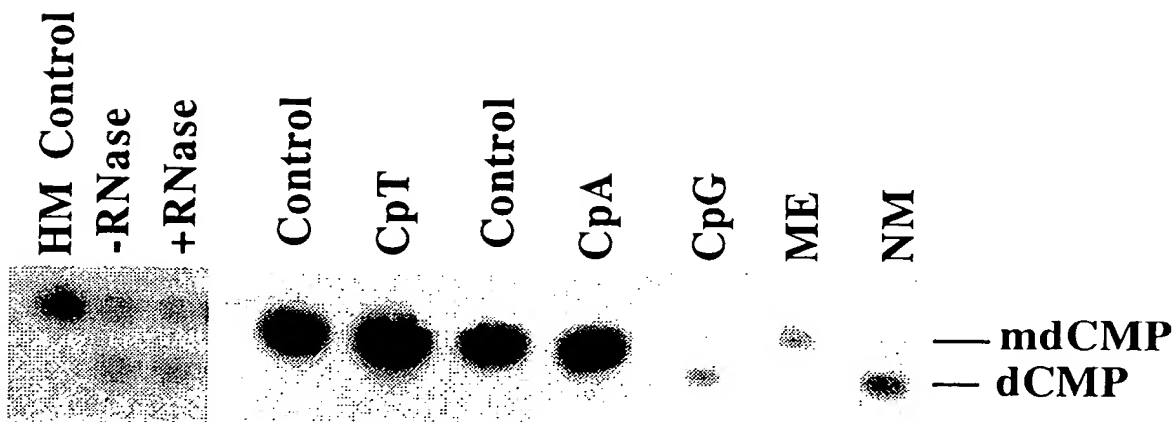
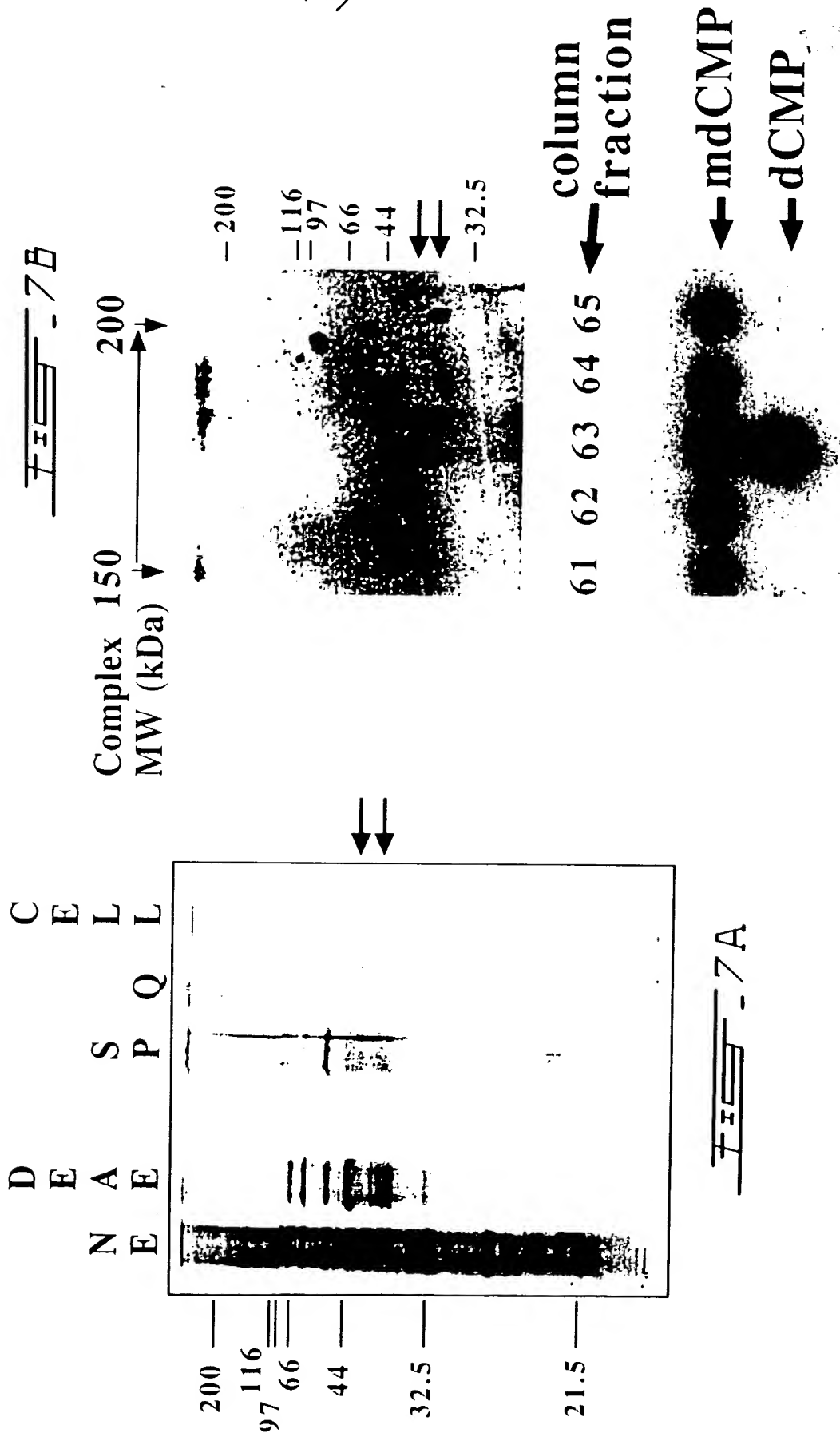


FIG. 1C



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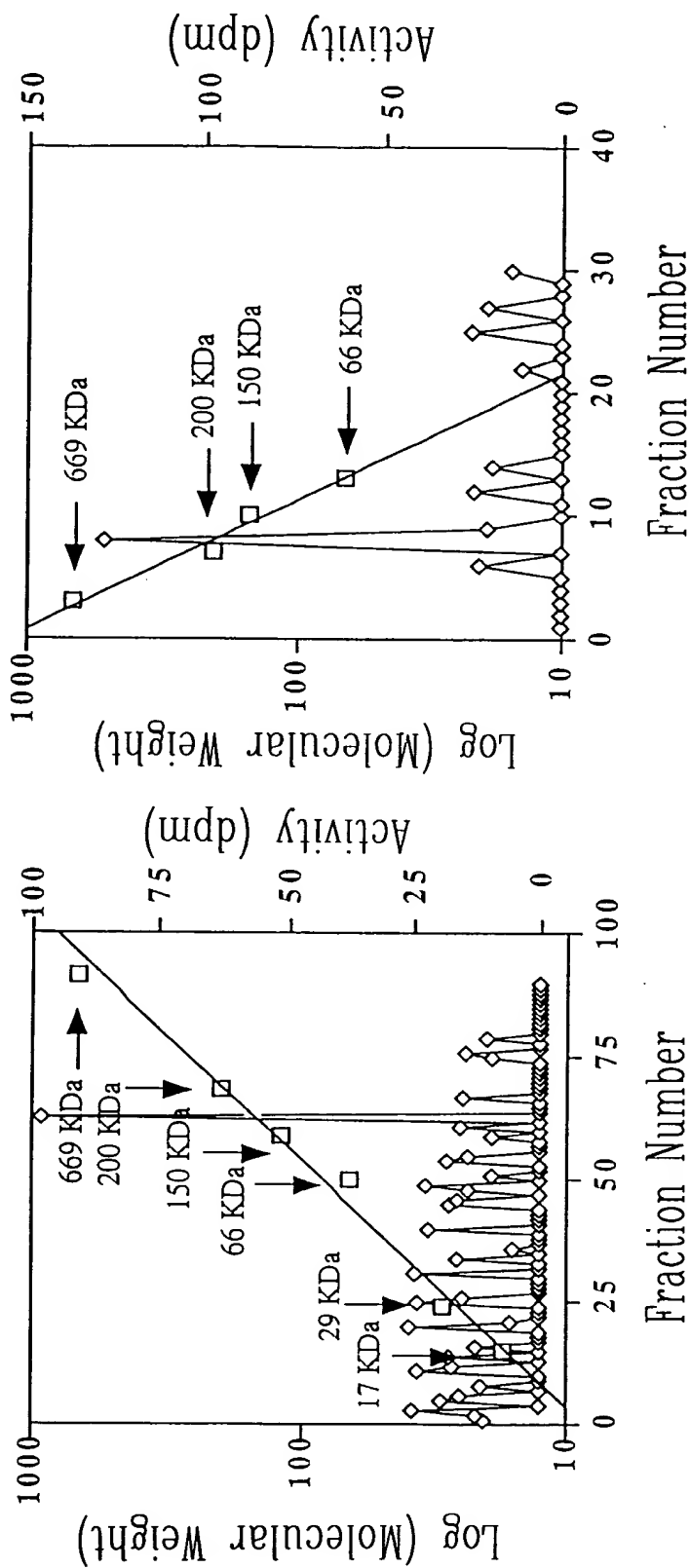


Fig - 7D

Fig - 7C



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EST DCPALPPGMKKEEVIRKSGLSAGKSDVYFSPSGKKFRSKPOLARYLGIVDLS  
|||||  
D P LP GW ++ RKSG SAGK DWY +P GK FRSK +L Y D S  
|||||  
MeCP2 15 DDPTLPEGWIRKLKQKSGFRSAGKYDVLINPQKAFRSKVELLAYFEKVGDTG 68

FEET - BA

MDCPALPPGM KKEEVIRKSG LSAGKSDVY FSPSGKKFRS	40	
KPOLARYLGN TVDLSSFD FR TCKMMP SKLQ KNKQRLRNDP	80	
LNQNKGKPD L NTTLP IRQTA SIFKQPVT KV TNHPSNKVKS	120	homology to methylated DNA binding domain
DPQRMNEQPR QLFWEKRLQG LSASDVTEQI IKTMELPKGL	160	
QGVGPGSND E TLLSAVASAL HTSSAPITGQ VSAAVEKNPA	200	homology to coiled coil domain
VWLNTSQPLC KAFIVTDEDI RKQEERVOOV RKILEDALMA	240	
DILSRAADTE EMDIEMDSGD EA	262	

FEET - BB



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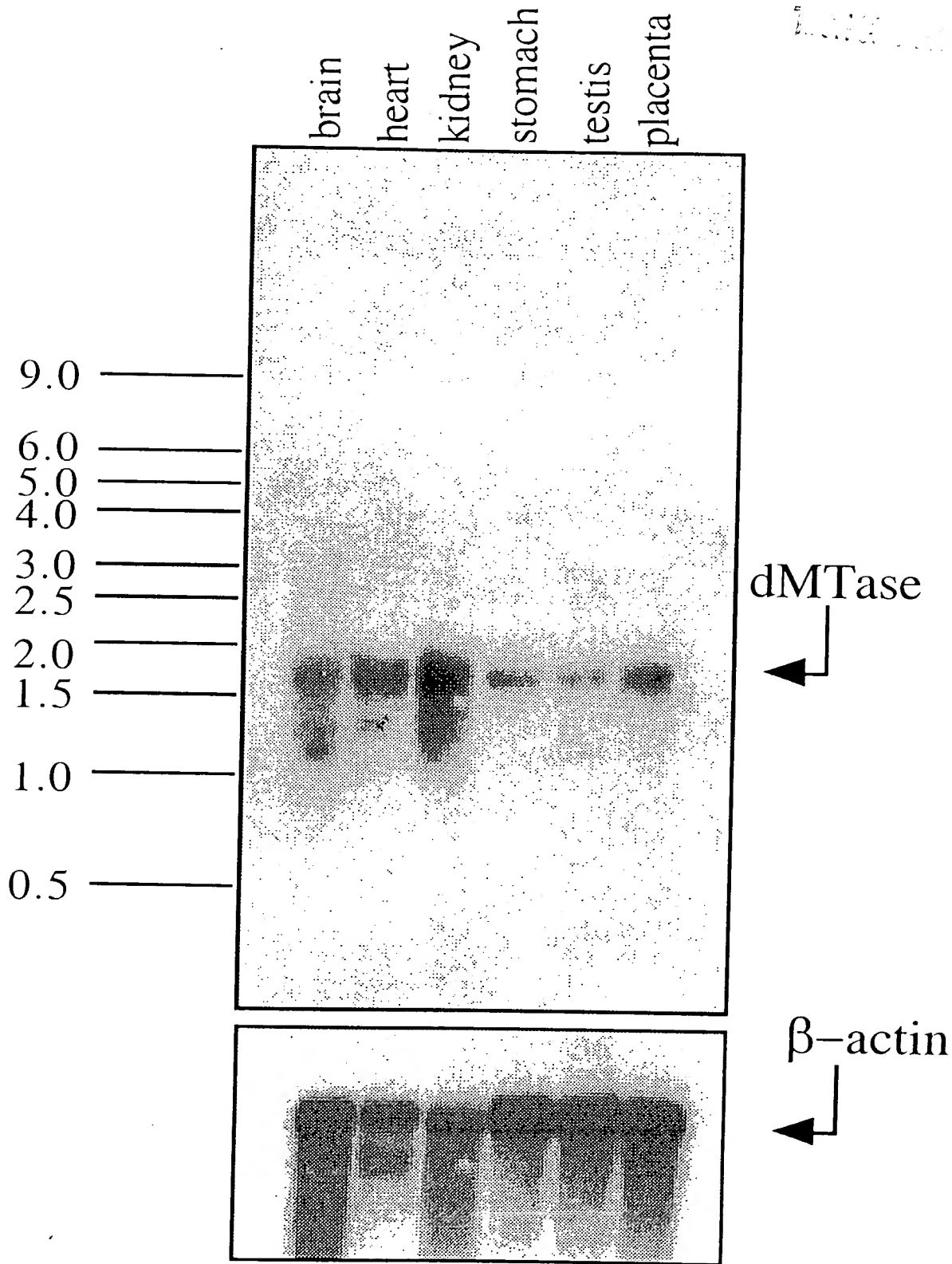


FIG. 8C



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# Human DNA demethylase cDNA-dMTase1 and predicted amino acid sequence

5' gggggcgctgg ccccgagaag gcggagacaa gatggccgcc catagcgctt ggaggaccta  
agagggcggctg gccggggcca cggcccgggc aggagggccg ctctgtgcgc gcccgctcta  
tgatgcttgc gcgcgtcccc cgcgcgccgc gctgcgggctt gggcgggtct ccgggattcc  
aagggctcgg ttacggaaga agcgcagcgc cggctgggga gggggctgga tgcgcgcgca  
cccgggggga ggcgcgtgct gcccgagca gagagtgagg gagagtgagg cgggcggcag  
cggcgtggc ggcgactccg ccatagaca ggggggcccag ggcagcgcgc tcgcccctc  
cccgtgagc ggcgtgcgca ggaaggcgc tcggggcggc gccgtggcc gggggcggctg  
gaagcaggcg gccggggcg ggcgcgtctg tggccgtggc cggggccggg gccgtggccg  
gggacgggga cggggccggg gccggggcgc cggcgtccc ccgagtgagg gcagcggcct  
tggcggcgac ggcggcggct gcggcggcg cggcagcggc ggcggcggcg ccccccggcg  
ggagccggtc ccttcccgt cggggagcgc ggggcgggg gccaggggac ccggggccac  
ggagagcggg aagaggatgg atggccggc cctcccccc ggatggaga aggaggaaagt  
gatccgaaaa tctgggctaa gtgctggcaa gagcgatgtc tactactca gtccaagtgg  
taagaagtcc agaagcaagc ctcagttggc aaggtacctg ggaaatactg ttgatctcag  
cagttttgac ttcagaactg gaaagatgat gcctagtaaa ttacagaaga acaaacagag  
actgcgaaac gatcctctca atcaaaataa gggtaaacca gacttgaata caacattgcc  
aattagacaa acagcatcaa ttttcaaca accggtaacc aaagtcacaa atcatcctag

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FIG. 1 - 9A



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taataaagtg aaatcagacc cacaacgaat gaatgaacag ccacgtcagc ttttctggga  
gaagaggcta caaggactta gtgcatcaga tgtaacagaa caaattataa aaaccatgga  
actaccctaa ggtcttcaag ggttgggtcc aggtagcaat gatgagaccc ttttatctgc  
tgttgccagt gctttgcaca caagctctgc gccaatcaca gggcaagtct ccgctgctgt  
ggaaaagaac cctgctgttt ggcttaacac atctcaacc ctctgcaaa cttttattgt  
cacagatgaa gacatcagga aacaggaaga gcgagtacag caagtacgca agaaattgga  
agaagcactg atggcagaca tctgtcgcg agctgctgat acagaagaga tggatatgga  
aatggacagt ggagatgaag cctaagaata tgatcaggta actttcgacc gactttcccc  
aagrgaaaat tcctagaaat tgaacaaaaa tgtttccact ggcttttgcc tgtaagaaaa  
aaaatgtacc cgagcacata gagcttttta atagcactaa ccaatgcctt ttagatgta  
tttttgatgt atatatctat tattcaaaaa atcatgttta ttttgagtcc taggacttaa  
aatagtctt ttgtaatatc aagcaggacc ctaagatgaa gctgagcttt tgatgccagg  
tgcaatctac tggaaatgta gacttacgt aaacatttg tttccccac agttttaata  
agaacagatc aggaattcta aataaatctc ccagttaaag attattgtga cttcactgta  
tataaacata tttttatct ttattgaaag gggacacctg tacattcttc catcatcact  
gtaagacaa ataaatgatt atattcaca aaaaaaaa 3'

SEQ ID NO:1

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MRAHPGGGCCPEEEGESAAAGSGAGGDSAIEQGGQSALAPSPVSGVR  
REGARGGGRGRWKQAGRGGVCGRGRGRGRGRGRGRGRGRPPSG  
GSGLGDDGGGGGGGAPRRREPVPFPGSAGPPRGPGRATESGKRM  
DCPALPPGWKKEEVIRKSGLSAGKSDVYFSPSGKKFRSKPQLARYLGNT  
VDLSSFDFRTGKMMPSKLQKNKQRLRNDPLNQNKGPDLNTTLPIRQTAS  
IFKQPVTKVTNHPSNKVKSDPQRMNEQPRQLFWEKRLQGLSASDVTEQII  
KTMELPKGLQGVPGSNDETLLSAVASALHTSSAPITGQVSAAVEKNPAV  
WLNTSQPLCKAFIVTDEDIRKQEEERVQQVRKKLEALMADILSRAADTEE  
MDIEMDSGDEA

SEQ ID NO:2

FIG. 1



SEP 20 2003

# Human DNA demethylase homologue-dMTase2 and predicted amino acid sequence

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5' agcgggccga ggagccgggc gcaatggagc ggaagaggtg ggagtgccgc gcgctcccgc  
agggctggga gagggagaa gtgccagaa ggtcggggct gtcggccggc cacagggatg  
tctttacta tagccgagc gggaagaagt tccgcagcaa gccgcagctg gcgcgctacc  
tgggcggctc catggacctg agcaccttcg acttcgcac gggcaagatg ctgatgagca  
agatgaacaa gagccgccag cgcgtgcgt acgactctc caaccaggtc aagggaagc  
ccgacctgaa cacggcgctg cccgtgcgc agacggcgtc catctcaag cagccggtga  
ccaagattac caaccaccc agcaacaagg tcaagagcga cccgcagaag gcggtggacc  
agccgcgcca gctcttctgg gagaagaagc tgagcggcct gaacgcctc gacattgctg  
aggagctggt caagaccatg gacctccca agggcctgca ggggtggga cctggctgca  
cggatgagac gctgctgtcg gccatcgca gcgccctgca cactagcacc atgcccatca  
cgggacagct ctggccgcc gtggagaaga acccggcgt atggctcaac accacgcagc  
ccctgtgcaa agccttcatg gtgaccgacg aggacatcag gaagcaggaa gagctggtgc  
agcagggtcg gaagcggctg gaggagcgc tgatggcga catgctggcg cacgtggagg  
agctggcccg tgacggggag gcgcgcgtgg acaaggcctg cgctgaggac gacgacgagg  
aagacgagga ggaggaggag gaggagccc gaggagccc accggacc ggagatggag cacgtctagg  
gcagagggcc tgccgagagc ccgtgctgcc cctggagcc gcctgcagac gcggtcctcg  
gcccacgtg aaccaggctc ggcggcgaag ccagccttg gagacacca ggaggaaagg  
cgtgctcctg gctccctcct cggcccgctc cacttccc ggccctcggg gcacacagct  
ggggctgccc ccacccgaaa gaccctccac gctcgtcctc tacagagtcc ggctcggga  
agtgcggggt gctcctgggc cctgcctggc tccctacgac ctttgggctc gagggcagct

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cctccccatg cccgctgtcc cagtccttg agactggaga gcagccagca ggtgccccgc  
agctcggcgc cacggcttgc tgacagctgg gaggtttct cggtctggag gcgtagtttt  
gaaactcaca tcaccactg tgcagcgtga ggacgggact ctggtctgct gtggggggca  
tgcaggacgg cgccactctc tgccctgcca tgcggctggt ggtgccacag agcctcacgg  
tgcctgagtg gcgtgccag ggaggccgct ctcttcagt aaatgtaaca cagtcgaggg  
acgtcatcgg gcagccttcc ctgtgtgcca acgccagcct tcgcttctga aaacaaact  
ccagccgctg ccagtcggga ctgtgtcgcc cggcgctgcc agaattgctcc actgccagcc  
ggccccctg cctcgggttc cttctgttt agtggcgaca caggcaccca gctttgggg  
ggtgctgacg ctcccagggg tgccaggagc cactgggaca ggttgaggct ccagacgct  
cctcgagtg ccagctctc cagggagctt ctggcccaag gcgttcttga gggatctgct  
ccttaacccc ccagtgcctt ggcgagggca ggttccaagc cacagacgcc tgccccgagt  
ggactttgcg gccagtccct ggggtgcctc ctgggccctg cttggccagt gagggttcct  
aacgggtggg ttcawtggcc tggcccvagc gagccccac ctgcattgac cttagggcca  
tagagagggc ctgtcccggc gctgccccag ccaaggatct ggtcgtgcc ccagggggac  
tgatggggcaa gagtgcgcc tgtggctgga ctgtgacct cctgatggg gcctgaccgc  
gggagctgag gaagcgccgc tccaccgtct gccctccaag gacccgcatg gaggcagtgg  
gctggcagct tcctgctgct ccctgtcaga gtcaaaagcac aaatcctcag gacgggctca  
agggccaggg cagccgaggg aagctccagg tggggaccac gtcttctga ggttggtgcc  
cactggctgg gaccctttgc agtgggggtg cctccccctc gtctgcctgg tggaggggagc  
cgtgggctg gggacgtgac tgaataaagc caccatgggt gg 3'

SEQ ID NO:3

FILE - BE



Serial No. 09/554,414  
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MERKRWECPALPQGWEREVPRRSGLSAGHRDVFYSPSGKKFRSKPQLA  
RYLGGSMDLSTFDFTGKMLMSKMNKSRQVRVYDSSNQVKGKPDNLNTALP  
VRQTASIFKQPVTKITNHPSNKVKSDPQKAVDQPRQLFWEKKLSGLNAFD  
IAEELVKTMDLPKGLQGVGPGCTDETLLSAIAASALHTSTMPITGQLSAAV  
EKNPGVWLNTTQPLCKAFMVTDEDIRKQEEELVQQVRKRLEEALMADMLAH  
VEELARDGEAPLDKACAEDDDDEDEEEEEPPDPPEMEHV

SEQ ID NO: 4

7-1-9F



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Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>411)		Seq2(1>291)		Similarity		Gap		Consensus	
human dMTase1 protein	human dMTase2 protein	human dMTase1 protein	human dMTase2 protein	Index	Index	Number	Length	Length	Length
(148>397)	(4>253)	(148>397)	(4>253)	76.0	76.0	0	0	0	250
(148>397)	(4>253)	(148>397)	(4>253)	76.0	76.0	0	0	0	250
v150	v160	v170	v180	v190	v200	v210			
KRMDCPALPPGWKKEEVIRKSGLSAGKSDVYFSPSGKKFRSKPQLARYLGNIVDLSSFDFTGKMMPSK									
KR :CPALP.GW.:FEV R:SGLSAG..DV:Y:SPSGKKFRSKPQLARYLG.:DLS:FDFTGKM: SK									
KRWECPALPQGWEREFEVPRRSGLSAGHRDVFYSPSGKKFRSKPQLARYLGGMDLSTFDFTGKMILMSK									
25/50									
^10 ^20 ^30 ^40 ^50 ^60 ^70									

v220	v230	v240	v250	v260	v270	v280
LQKNKQRLRNDPLNQKGPDLNTTLPIRQTASIFKQPVTKVINHPNKNVKSQDPQRMNEQPRQLFWEKRL						
::K::QR:R D: NQ KGKPDINT:LP:RQTASIFKQPVTK:TNHPNKNVKSQDPQ: :QPRQLFWEK:L						
MNKSQRVRDSSNQVKGPDLNTALPVRQTASIFKQPVTKITINHPNKNVKSQDPQKAVDQPRQLFWEKKL						
^80 ^90 ^100 ^110 ^120 ^130 ^140						

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v290	v300	v310	v320	v330	v340	v350
QGLSADVTEQIIKIMELPKGLQGVGPGSND EITLSA/ASALHTSSAPITGQVSAAVEKNP						PAVWLNTSQP
GL:A D::E:::KIM:LPKGLQGVGPG..DEITLSA:ASALHTS: PITGQ:SAAVEKNP:VWLNT:QP						
SGLNAFDIAEELVKIMDLPKGLQGVGPGCTDEITLSA/ASALHTSIMPITGQLSAAVEKNP						GVWLNTITQP
^150	^160	^170	^180	^190	^200	^210
v360	v370	v380	v390			
LCKAFIVTDEDIRKQEEERVQQVRKLEEFALMADILSRAAD						
LCKAF:VIDEDIRKQEE VQQVRK:LEEFALMAD:L::::						
LCKAFMVIDEDIRKQEEELVQQVRKLEEFALMADMLAHVEE						
^220	^230	^240	^250			



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# Mouse DNA demethylase-dMTase1 and predicted amino acid sequence

5' ccgctctgcg ggcggggcgcg gtctccggga ttccaaggcg tcggttacgg aagaagcgca  
gagccggctg gggagggggcg tggatgcgcg cgcacccggg gggaggccgc tgctgcccgg  
agcaggagga gggggagagc gcggcgggcg gcagcggcg cgtccccggt gagcggcgtg cgcagggaag  
agcagggggg ccagggcagc gcgctcgctc ggcggggggc ggtggaagca ggcggcccg ggcggcgcg  
gcgctcgggg tggccgtggc cgtggcgggg gtcggggcg gtcggggggc ggcggcgcg  
gcccggcgcg tcccagagt ggcggcagc ggtggcgcg ggcggcgcg gccttggcg cgcggcggc  
gcggtgcgcg cgtcggcagc ggcggcgcg ggcggcgcg ggcggcgcg ggcggcgcg ggcggcgcg  
cgtcggggag ctcggggcg ggcggcgcg ggcggcgcg ggcggcgcg ggcggcgcg ggcggcgcg  
tggactgccc ggcctcccc caagagcgat gtctactact ctgggaaatg ctgttgacct tagcagtgtt gacttcagga  
aacctcagct ggcaagatag gatgcctagt aaattacaga agaacaagca gagactccgg aatgaccccc  
ccaatcagaa caagggtaaa ccagacctga acacaacatt gccaataga caaactgcat  
caattttcaa gcaaccagta accaaattca cgaaccacc gagcaataag gtgaagtcag  
acccccagcg gatgaatgaa caaccacgtc agcttttctg ggagaagagg ctacaaggac  
ttagcgcac agatgtaaca gaacaaatta taaaaccat ggagctacct aaaggtcttc  
aaggagtcgg tccaggtagc aatgacgaga cccttctgtc tgctgtggcg agtgctttac

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FIG. 1



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acacaagctc tgcgcccac acaggacaag tctctgctgc cgtggaaaag aaccctgctg  
tttggcttaa cacatctcaa cccctctgca aagctttcat tgttacagat gaagacatta  
ggaacacagga agagcgagtc caacaagtac gacaaggagg aagtagacat ggaggaggca ctgatggccg  
acatcctgtc ccgggctgag gacacggagg aagtagacat tgacatggac agtggagatg  
aggcgtaaga atatgatcag gtaactttcg actgacctc cccaagagca aattgctaga  
aacagaatta aaacatttcc actgggttcc gcctgtaaga aaaagtgtac ctgagcacat  
agctttttaa tagcactaac caatgccttt ttagatgtat ttttgatgta tatacttatt  
attccaaatg atgtttattt tgaatcctag gacttaaaat gactctttta taatagcaag  
cagggccctt ccggtgcagt gcagctttga ggccagggtgc agtctactgg aaaggtagca  
cttacgtgaa atatttgttt cccccacagt tttaataataa acagatcagg agtaccaaat  
aagtttccca attaaagatt attatacttc actgtatata aacagatttt tatactttat  
tgaaagaaga tacctgtaca ttcttccatc atcactgtaa agacaaataa atgactatat  
tcac 3'

SEQ ID NO:5

FIG. 1 - 9J





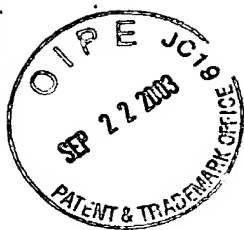
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# Mouse DNA demethylase-dMTase2 and predicted amino acid sequence

5' cacgcgcggg cgggtgggcg gagcgcccc ctagcgggg gctgtgaagc gcgggggaggg  
ggccgagcgg gtggcgaaagc cggcgcgcg cggctgggg gcggaggcg gagggccgtg  
ggacagaaca gctgcggcga gtggcggcgg cggagggagc cgaatcggcg acgagcccgg  
gggtcgcaac ttgcagaagc ggcgcgcgcg gcggcatcgg ccacggcggg cggaaaagcc  
ggggcgcaat ggagcggaag aggtgggagt gcccgcgct ccgcaggcg tgggaaaggg  
aagaagtgcc caggaggctg gggctgtcgg ccggccacag ggatgtcttt tactatagcc  
ccagcgggaa gaagtccgc agcaagccac aactggcacg ttacctgggc ggatccatgg  
acctcagcac cttcgacttc cgcaccggaa agatgttgat gaacaagatg aataagagtc  
gccagcgtgt gcgctatgat tctccaacc aggtcaaggg caagcctgac ctgaacaccg  
cgctgcctgt acggcagact gcatccatct tcaagcaacc ggtgaccaag atcaccaacc  
acccagcaa caaggtcaag agcaccgcg agaaggcagt ggaccagccg aggcagcttt  
tctgggagaa gaagctaagt ggattgagtg cctttgacat tgcagaagaa ctggtcagga  
ccatggactt gcccaaggcg ctgcaggagg tgggccctgg cttacacagc gagacgctgc  
tgtcagccat tgcgagtgtt ctacacacca gcaccctgcc cattacaggc cagctctctg  
cagccgtgga gaagaaccct ggtgtgtggc tgaacactgc acagccactg tgcaaaagcct  
tcatggtgac agatgacgac atcaggaagc aggaggagct ggtacagcag gtacggaagc  
gcctggagga ggcactgatg gccgacatgc tagctcatgt ggaggagctt gcccgagacg  
gggaggcacc actggacaag gcctgtgcag aggaggaaga ggaggaggaa gaggaggagg

FIG. 1



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SEQ ID NO:7

FILE - 9M

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aagagccgga gccagagcga gtgtagcaca ggtgccctgc ccaagtctgg gctgcagact  
gccttcagcc ttgcctggac caggtagggg ccagacctgt aggaggcagc cgtccacctc  
ctttccaaag cctcctgctt ccagggtctca gtgcaggagg cccctgtgga ccttgaactc  
acttgtccct gcgctgcctg gcaggaagcc ccacactgaa agcagatgag cagtgaccca  
actgagaggc cacctggaca cagtcacctc cctgcctcct tatcatagga caaggccttg  
cttggcaccc aggagctggg agccgtgttg ggtgctggag gaagtctctg gaaacacacc  
tggctatgcc caccttatgt ccctaaggct attacaggcc agggtttggg ctgctccggc  
ccacagggct gccagcctc ccacactga gggtcagcag ccaccaggga agtcacttct  
cttcaataaa ctgatggtag gaacttgtg 3'



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MERKRWECPALPQGWEREEVPRRSGLSAGHRDVFYSPSGKKFRSKPQLA  
RYLGGSMDLSTFDFTGKMLMNKMNKSRQRVRYDSSNQVKGPDLNTALP  
VRQTASIFKQPVTKI TNHPSNVKSDPQKAVDQPRQLFWEKKLSGLSAFD  
IAEELVRTMDLPKGLQGVGPGCTDETLLSAIASALHTSTLPITGQLSAAV  
EKNPGVWLNTAQPLCKAFMVTDDDIRKQEELVQQVRKRLEEEALMADMLAH  
VEELARDGEAPLDKACAEFFFFFFFFEEEEPEPERV

SEQ ID NO: 8

FIG. 1 - 9N



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Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>414)

Seq2(1>285)

mouse dMTase2 protein

Similarity

Gap Number

Gap Length

Consensus Length

mouse dMTase1 protein  
(151>400)

(4>253)

75.2

0

0

250

(151>400)

(4>253)

75.2

0

0

250

v160 v170 v180 v190 v200 v210 v220  
KRMDCPALPPGWNKKEEVIRKSGLSAGKSDVYFSPSGKKFRSKPQLARYLGNVAVDLSSDFRTGKMMPSK  
KR :CPALP.GW.:EEV R:SGLSAG..DV:Y:SPSGKKFRSKPQLARYLG.:DLS:FDFTGKM: :K  
KRWECPALPQGWEREEVPRRSGLSAGHRDVFYSPSGKKFRSKPQLARYLGGSMDSLSTFDFTGKMLMNK  
^10 ^20 ^30 ^40 ^50 ^60 ^70  
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v230

v240

v250

v260

v270

v280

v290

LQKNKQRLRNDPLNQNKGKPDNLNITLPIRQTASIFKQPVTKFTNHPSNKKVKSDFQRMNEQPRQLFWEKRL  
::K::QR:R D: NQ KGKPDINT:LP:RQTASIFKQPVTK:TNHPSNKKVKSDFQ: :QPRQLFWEK:L  
MNKSRQVRDYDSSNQKGKPDINTALFVRQTASIFKQPVTKITNHPSNKKVKSDFQKAVDQPRQLFWEKKL  
^80 ^90 ^100 ^110 ^120 ^130 ^140

715-90



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v300 v310 v320 v330 v340 v350 v360  
QGLSASDVTEQIITIMELPKGLQGVGPGSNDITLLSAVASALHTSSAPITIGQVSAAVEKNPAAVWLNITSQP  
GLSA D::E:::TM:LPGGLQGVGPG..DETLLSA:ASALHTS: PITGQ:SAAVEKNP:VWINT:QP  
SGLSAFDIAEELVRIMDLPKGLQGVGPGCIDETLLSAIASALHTSTLPTITGQLSAAVEKNPVGWLNITAQP  
^150 ^160 ^170 ^180 ^190 ^200 ^210

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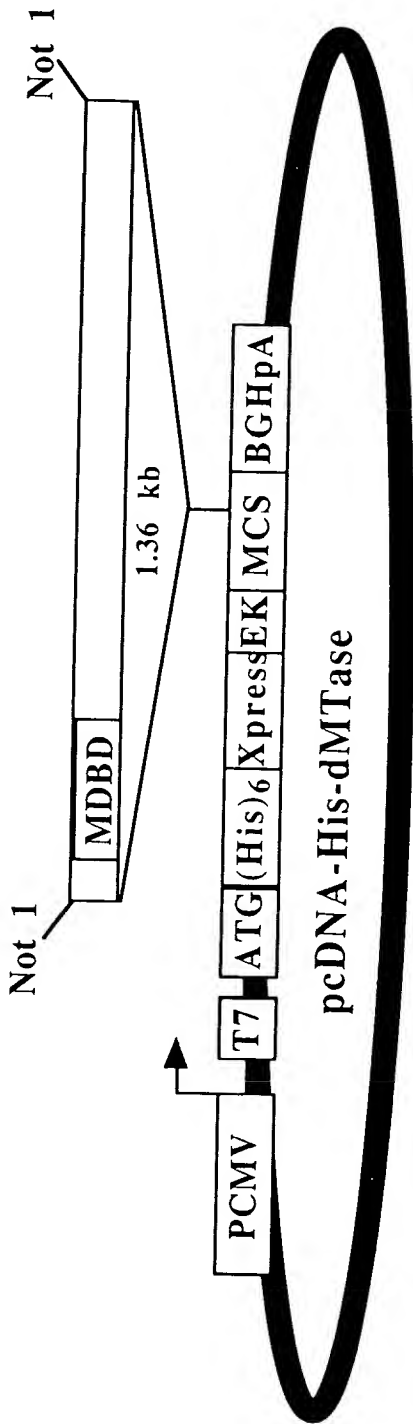
v370 v380 v390 v400  
LCKAFIVTDEDIRKQEEERVQQVRKKLEFALMADILSRAAD  
LCKAF:VTD:DIRKQEE VQQVRK:LEFALMAD:L:::  
LCKAFMVTDDDIRKQEEELVQQVRKRLLEFALMADMLAHVEE  
^220 ^230 ^240 ^250

FILED - 9 P



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miframe  
dMTase

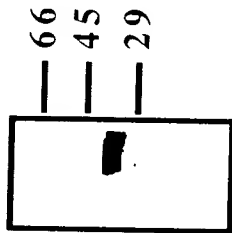


Fig. 10A



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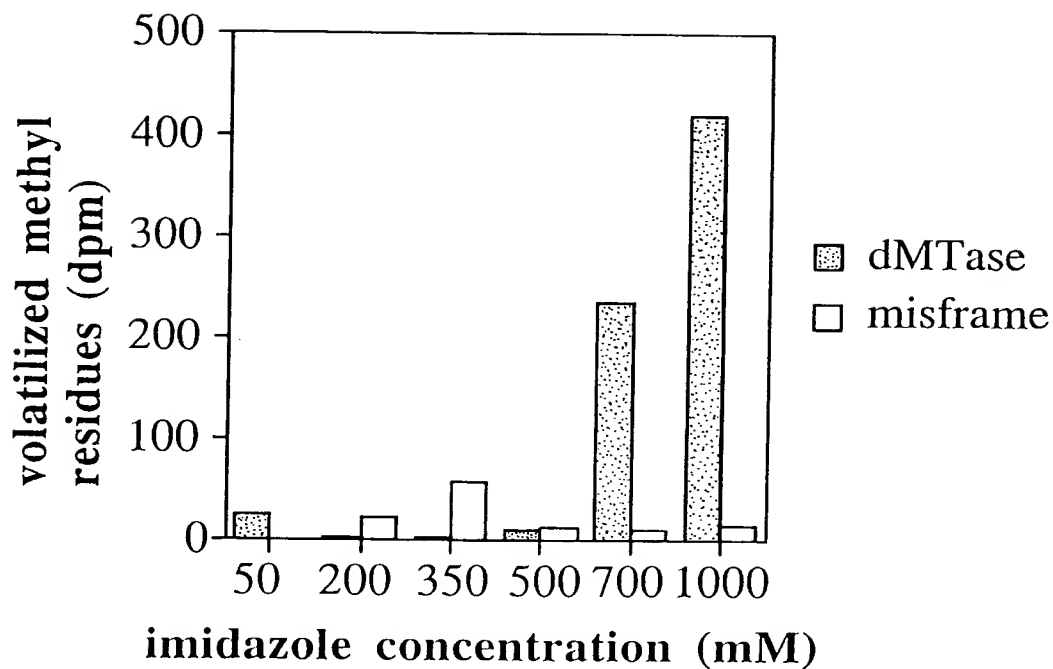
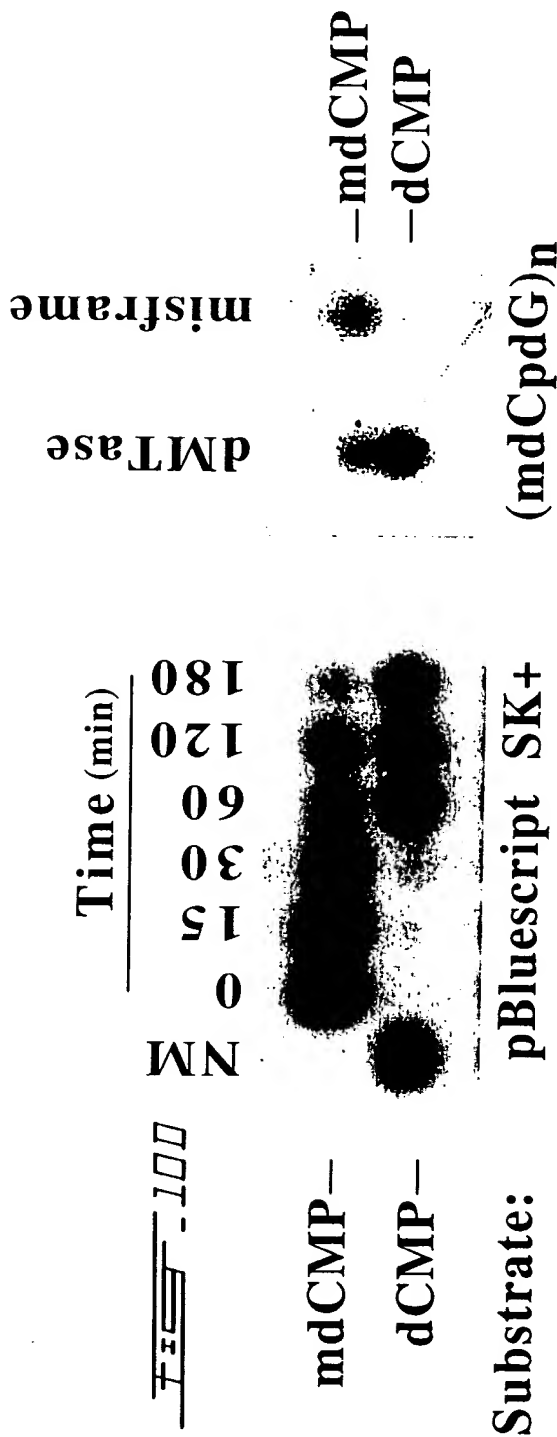
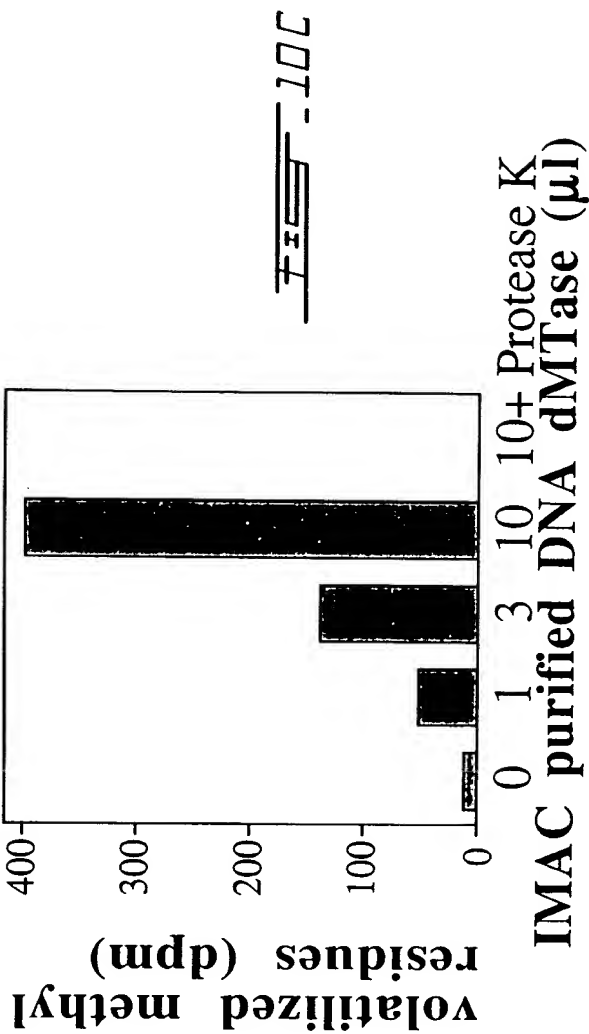


FIG. 10B



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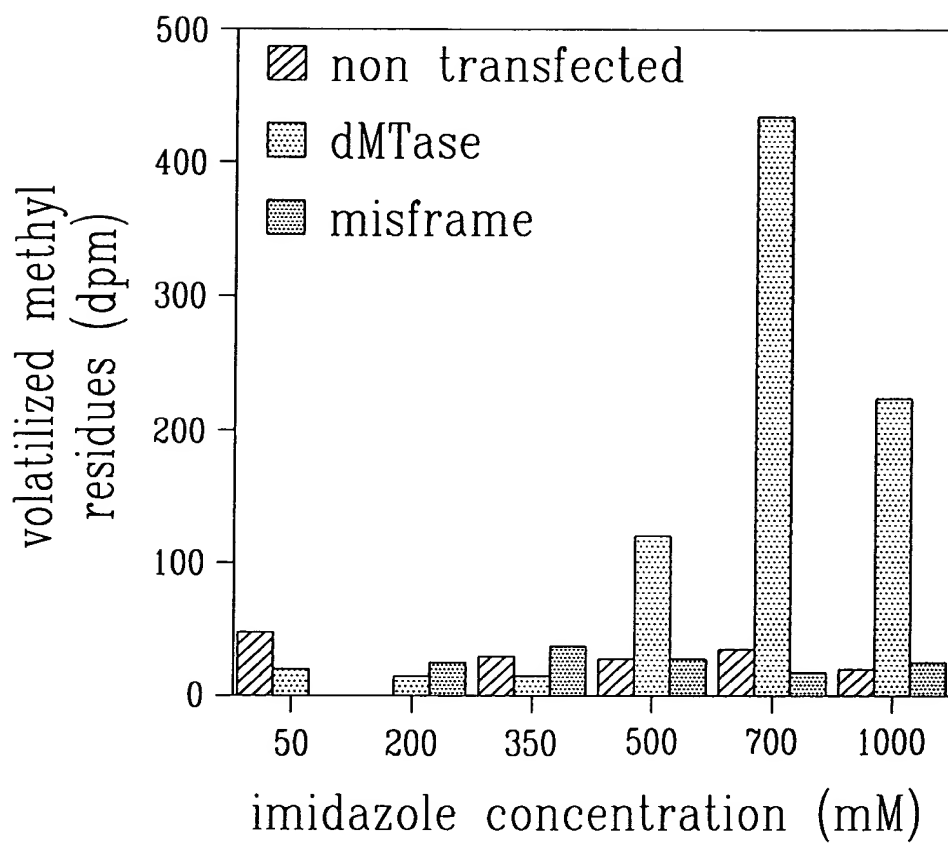
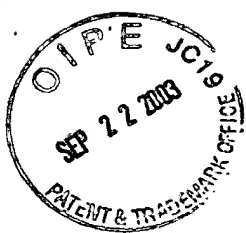
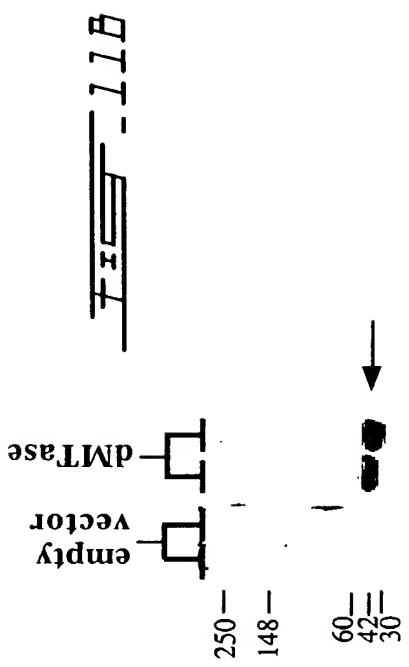


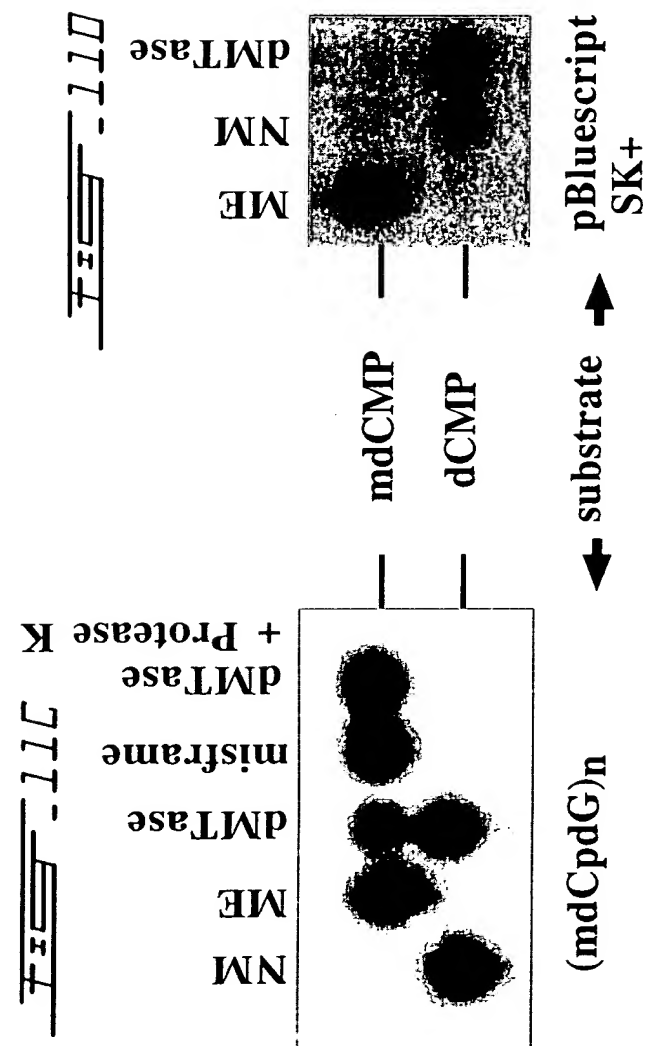
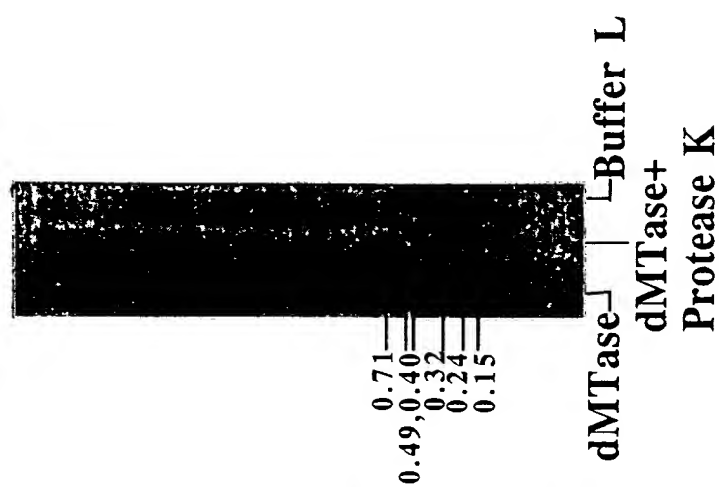
Fig. 11A



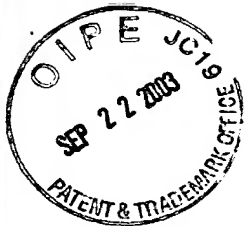
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**Figure 111E**  
me SK + Hpa II



(mdCpdG)<sub>n</sub>



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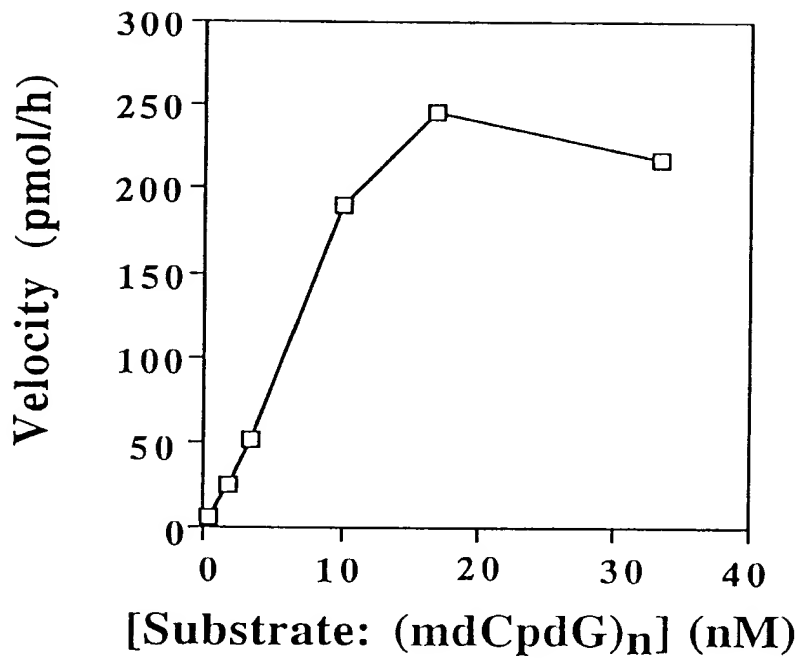


FIG-11F

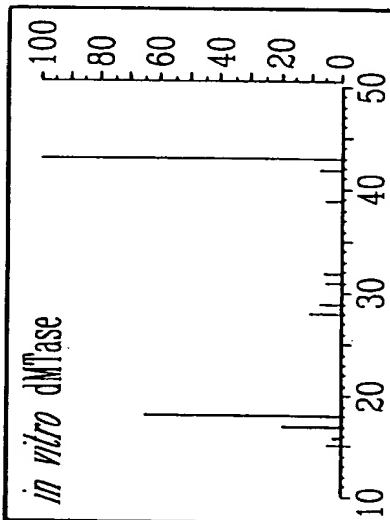
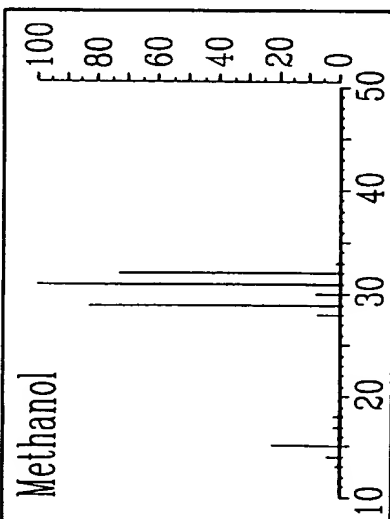
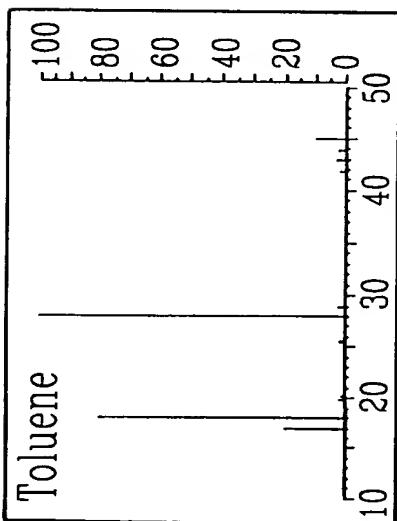
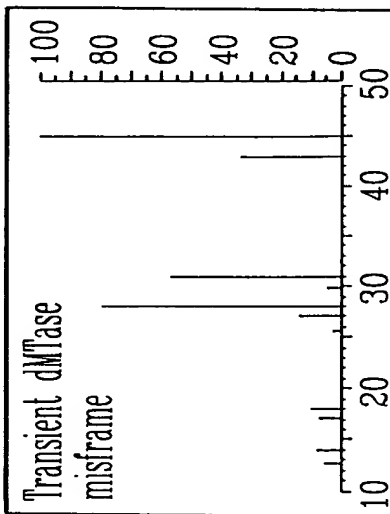
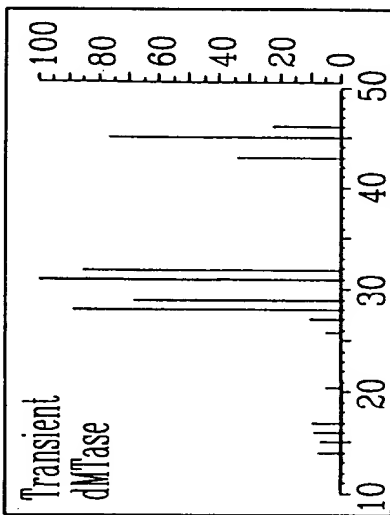
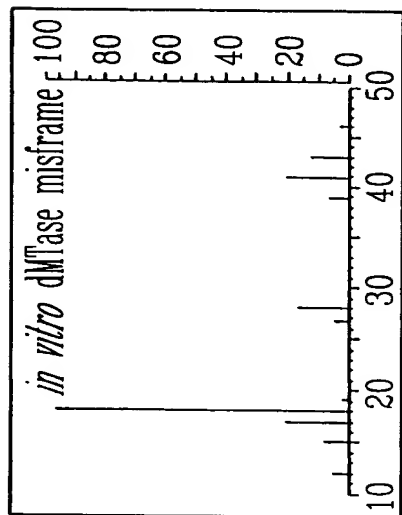
Serial No. 09/554,414  
REPLACEMENT SHEET



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Free - 12B





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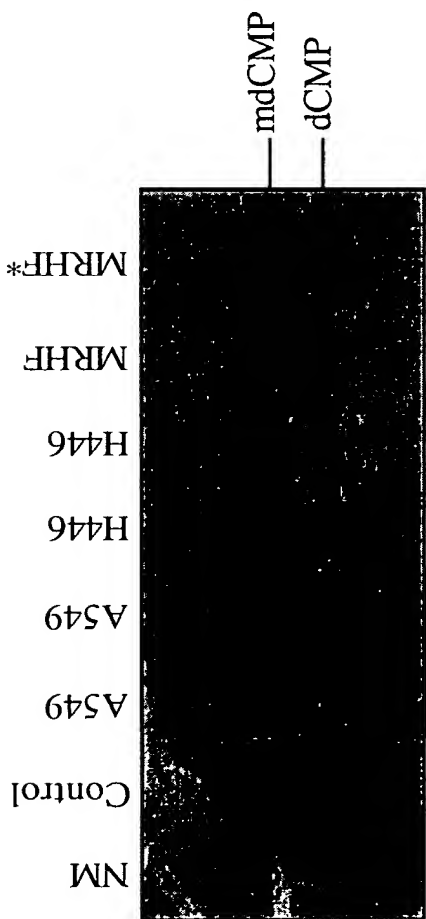
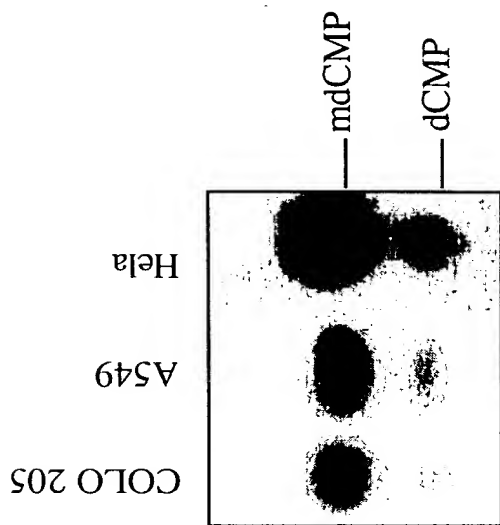
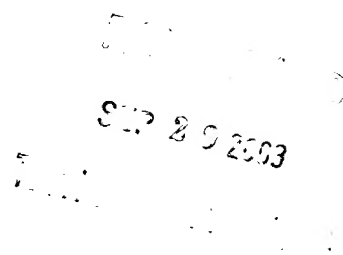


Fig. 13A

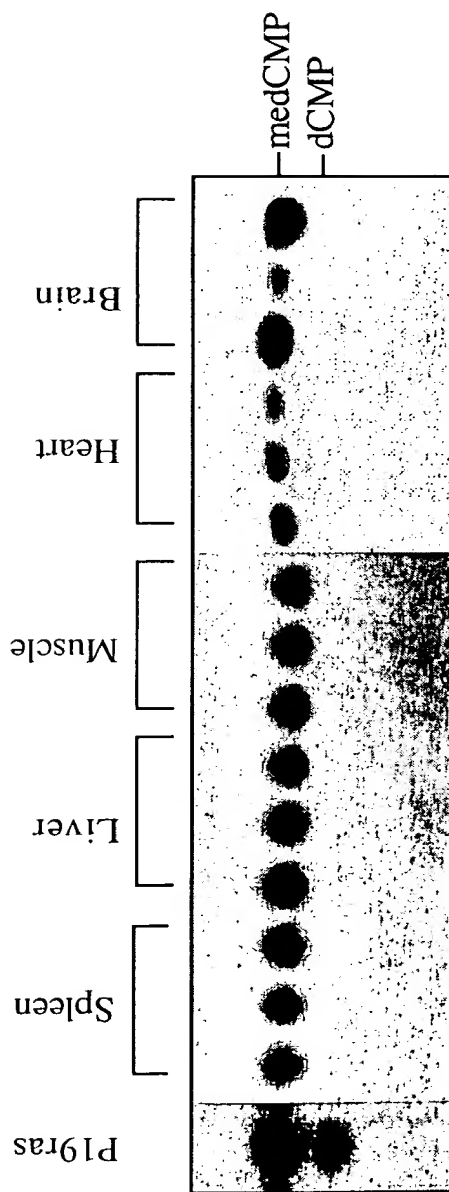


Fig. 13B



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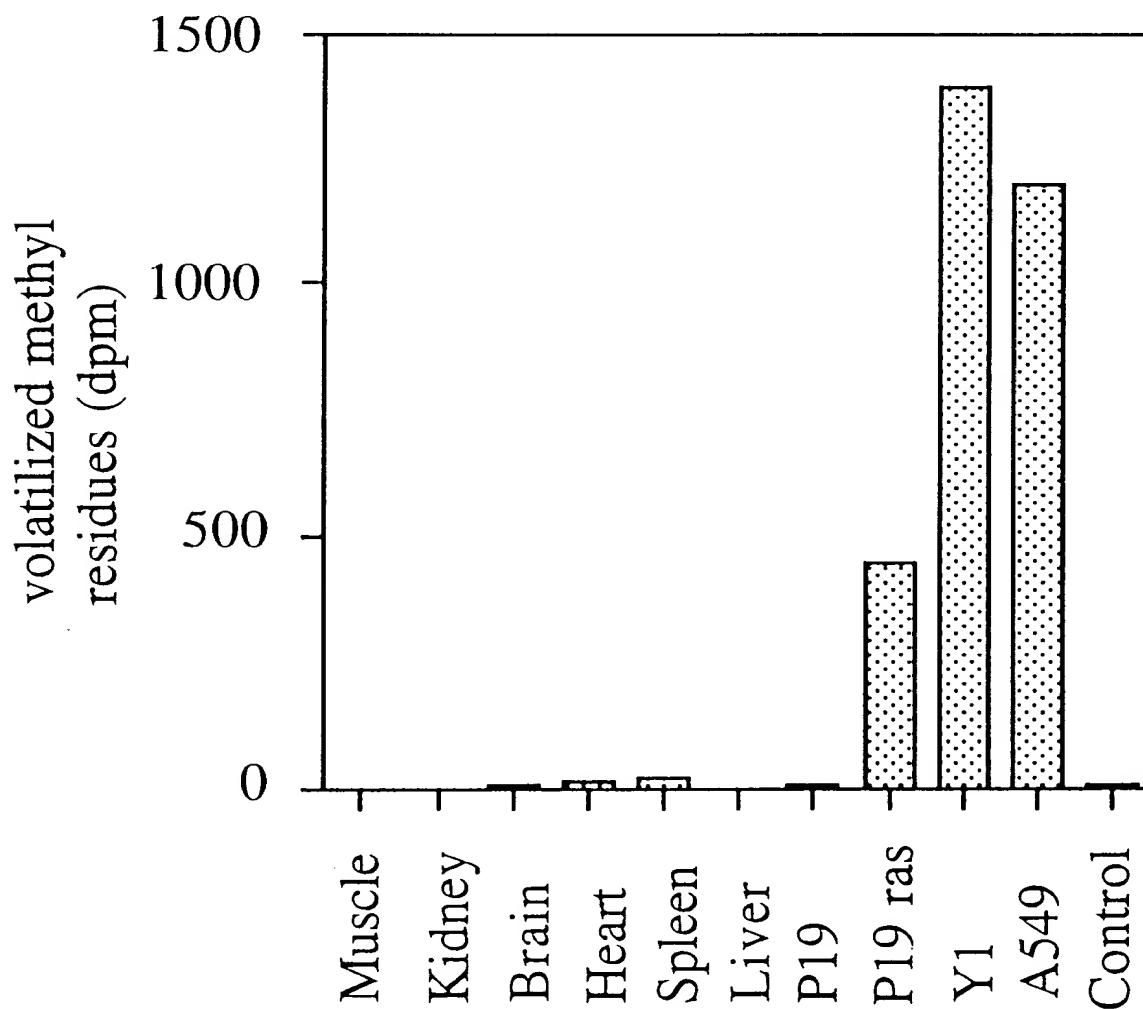


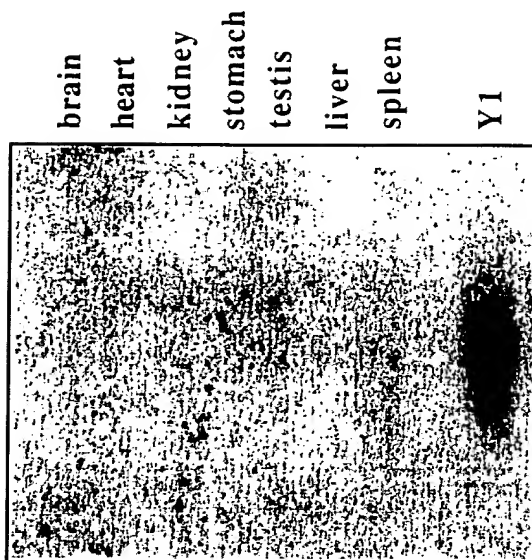
FIG. 13C



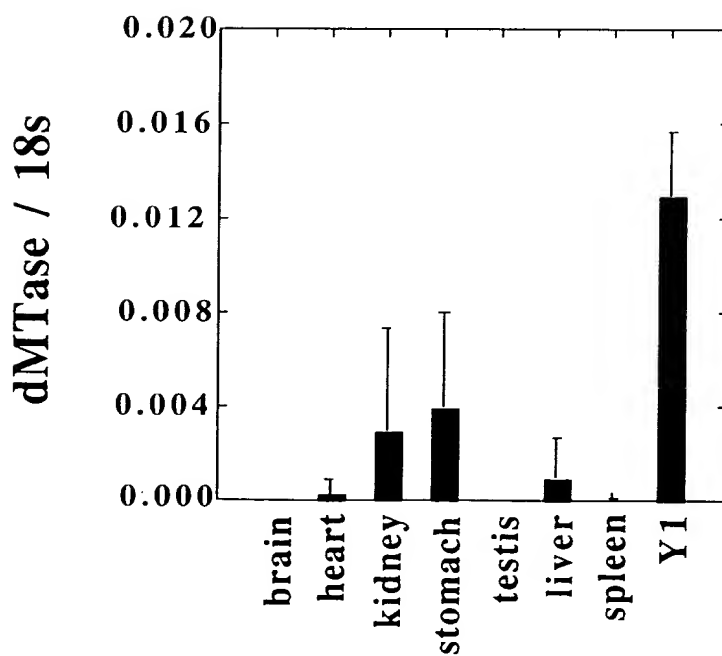
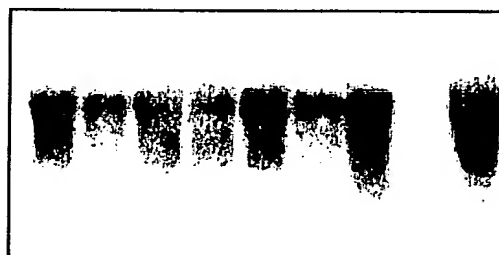
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dMTase



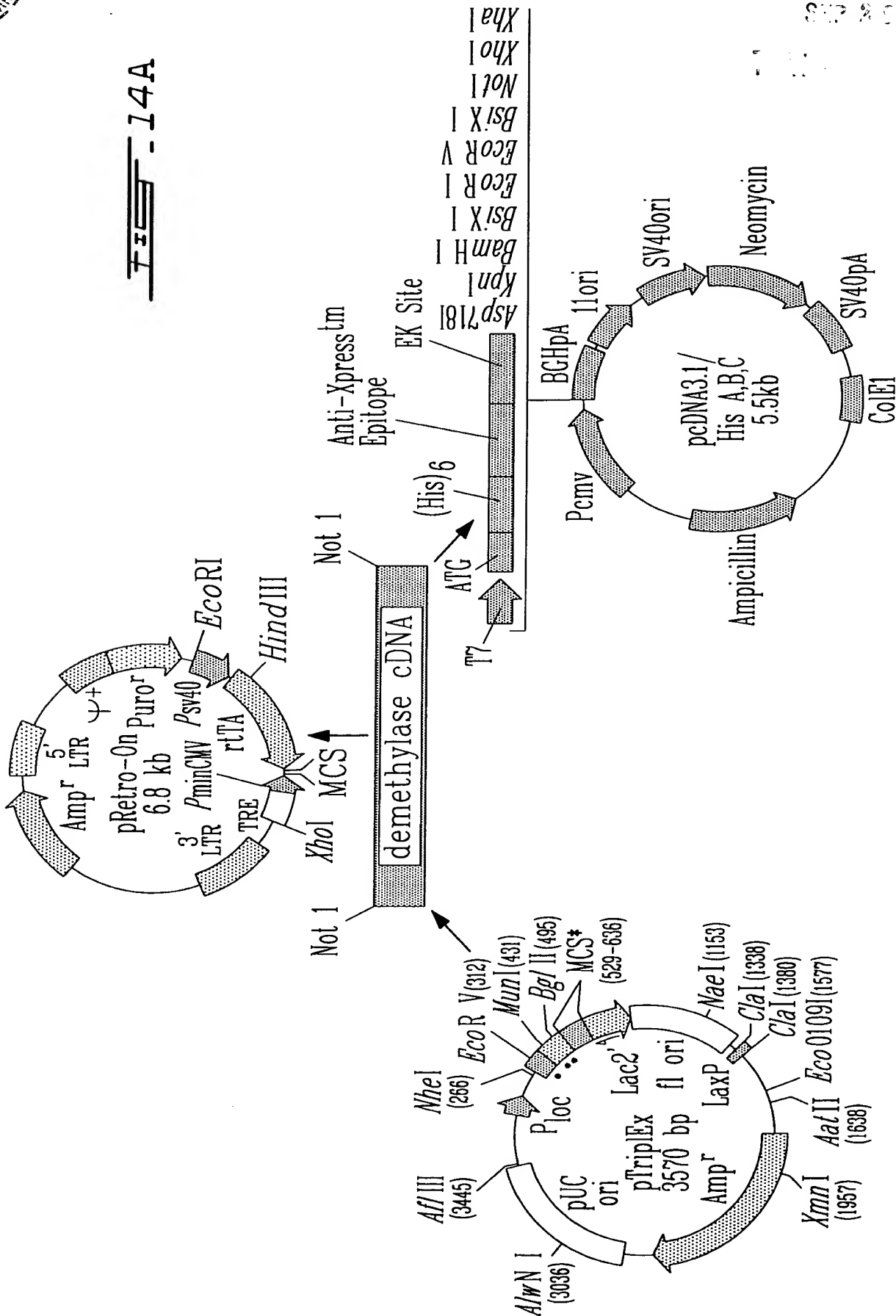
18s



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**FIG. 14A**





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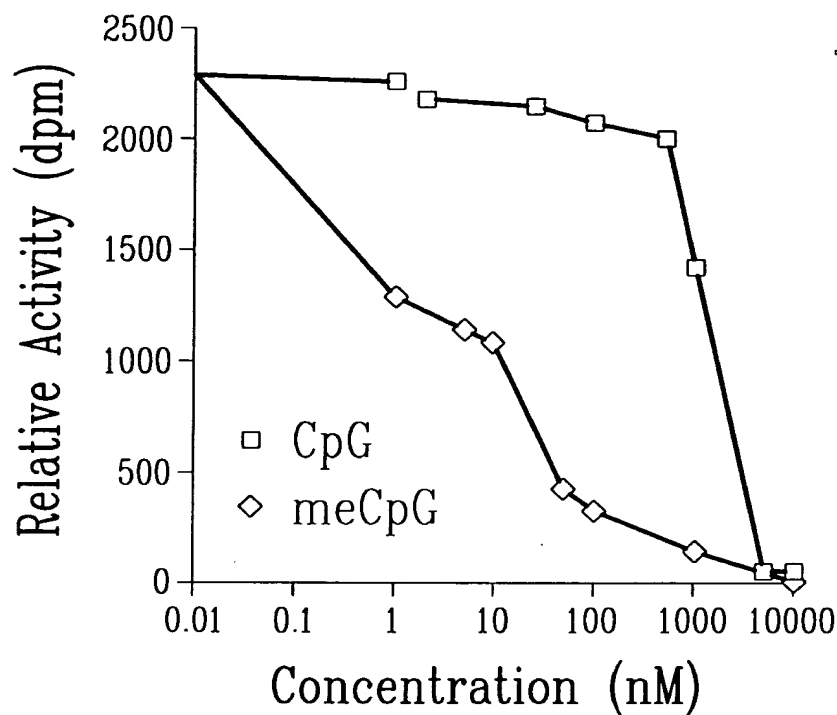


FIG. 14B

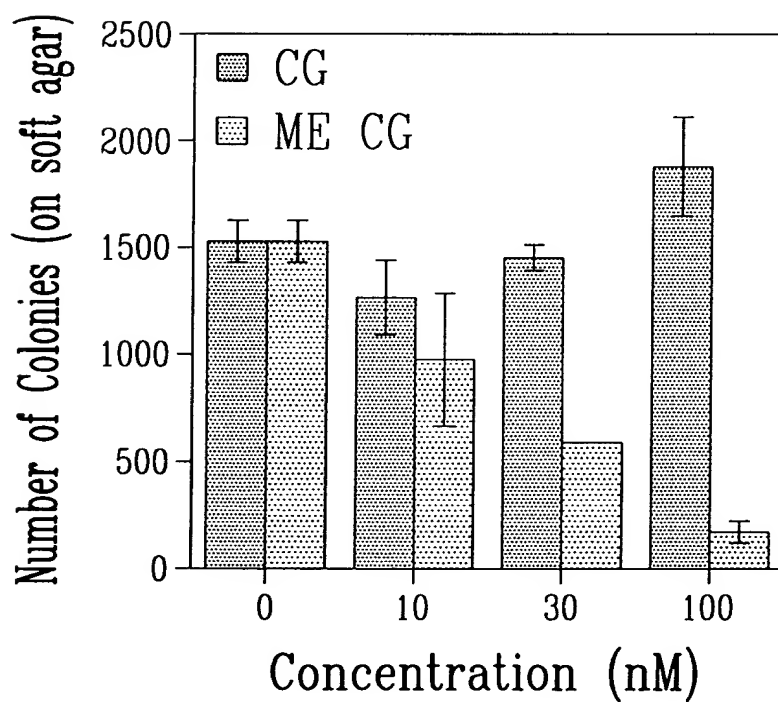
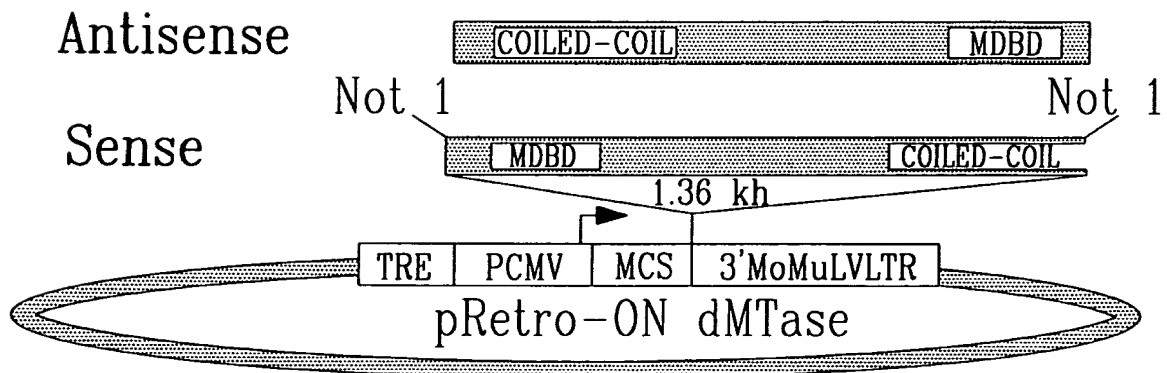
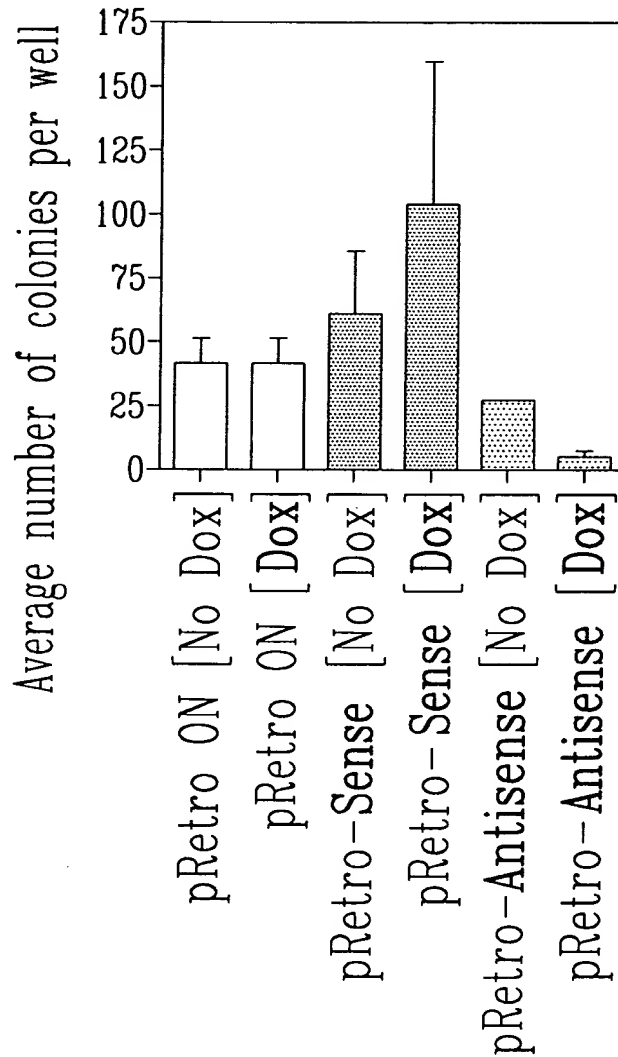


FIG. 14C

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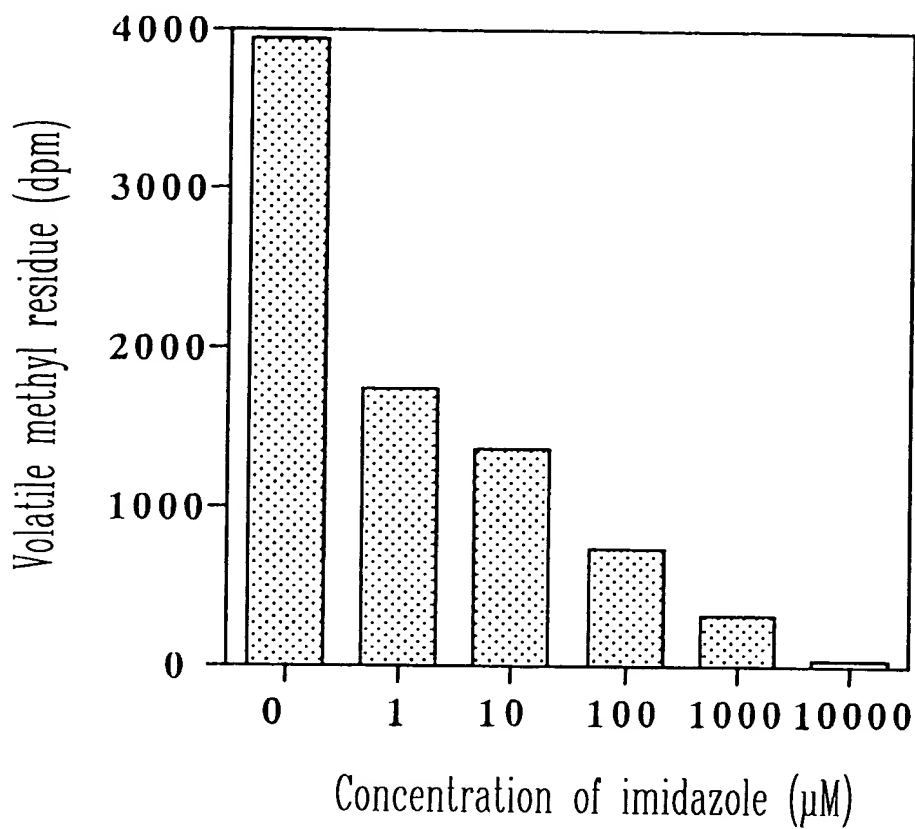


FIG. 16



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